

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2003, 20:57:11 ; Search time 107 seconds
(without alignments)
4944.088 Million cell updates/sec

Title: US-09-623-034-1
1725
Sequence: 1 tatatacacatagtctca.....gagcaaaagacttggtata 1725

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2-6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2-6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2-6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2-6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2-6/ptodata/2/ina/PCUTUS_COMB.seq:*
6: /cgn2-6/ptodata/2/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	552	32.0	1544	2	US-08-837-593-1	Sequence 1, Appl1
2	233	13.5	1467	1	US-08-176-620A-3	Sequence 3, Appl1
3	233	13.5	1467	1	US-08-463-862-3	Sequence 3, Appl1
4	233	13.5	1467	2	US-08-461-885-3	Sequence 3, Appl1
5	233	13.5	1467	2	US-08-458-887-3	Sequence 3, Appl1
6	233	13.5	1467	4	US-08-932-787B-3	Sequence 3, Appl1
7	233	13.5	1467	4	US-08-932-012C-3	Sequence 3, Appl1
8	233	13.5	1467	4	US-08-888-818C-3	Sequence 3, Appl1
9	232	13.4	1100	2	US-08-950-449A-18	Sequence 18, Appl1
10	232	13.4	3774	2	US-08-950-449A-11	Sequence 11, Appl1
11	232	13.4	3813	1	US-08-469-421-11	Sequence 11, Appl1
12	232	13.4	3813	1	US-08-250-975-11	Sequence 11, Appl1
13	232	13.4	3813	2	US-08-605-002A-11	Sequence 11, Appl1
14	232	13.4	3813	4	US-08-943-353-11	Sequence 11, Appl1
15	232	13.4	3813	5	PCT-US94-10529-11	Sequence 11, Appl1
16	230.4	13.4	1381	2	US-08-950-449A-13	Sequence 13, Appl1
17	230.4	13.4	1423	1	US-08-469-421-13	Sequence 13, Appl1
18	230.4	13.4	1423	1	US-08-250-975-13	Sequence 13, Appl1
19	230.4	13.4	1423	2	US-08-605-002A-13	Sequence 13, Appl1
20	230.4	13.4	1423	4	US-08-943-353-13	Sequence 13, Appl1
21	230.4	13.4	1423	5	PCT-US94-10529-13	Sequence 13, Appl1
22	230.4	13.4	1539	3	US-09-286-904-1	Sequence 1, Appl1
23	230.4	13.4	1539	4	US-09-640-101-1	Sequence 1, Appl1
24	222.2	12.9	1611	3	US-08-909-742-2	Sequence 2, Appl1
25	222.2	12.9	1611	4	US-09-412-289-2	Sequence 2, Appl1
26	220.8	12.8	3132	3	US-09-286-904-45	Sequence 45, Appl1
27	220.8	12.8	3132	4	US-09-640-101-45	Sequence 45, Appl1

28	212.2	12.3	2624	1	US-08-032-382B-1	Sequence 1, Appl1
29	209.4	12.1	1747	1	US-08-176-620A-1	Sequence 1, Appl1
30	209.4	12.1	1747	1	US-08-463-862-1	Sequence 1, Appl1
31	209.4	12.1	1747	2	US-08-461-985-1	Sequence 1, Appl1
32	209.4	12.1	1747	2	US-08-458-887-1	Sequence 1, Appl1
33	209.4	12.1	1747	4	US-08-932-787B-1	Sequence 1, Appl1
34	209.4	12.1	1747	4	US-08-932-012C-1	Sequence 1, Appl1
35	209.4	12.1	1747	4	US-08-888-818C-1	Sequence 1, Appl1
36	209.4	12.1	1866	3	US-08-909-742-1	Sequence 1, Appl1
37	209.4	12.1	1866	4	US-09-412-289-1	Sequence 1, Appl1
38	185.4	10.7	1023	3	US-08-554-385-4	Sequence 4, Appl1
39	183.8	10.7	1200	1	US-08-011-398B-3	Sequence 3, Appl1
40	183.8	10.7	1200	1	US-08-464-051-3	Sequence 3, Appl1
41	183.8	10.7	1200	2	US-08-462-498-3	Sequence 3, Appl1
42	170.2	9.9	1851	1	US-08-674-612-1	Sequence 1, Appl1
43	170.2	9.9	1851	1	US-08-700-575-45	Sequence 1, Appl1
44	170.2	9.9	1851	2	US-08-920-296-1	Sequence 1, Appl1
45	170.2	9.9	1851	4	US-09-124-163-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-837-593-1
Sequence 1, Application US/08837593
Patent No. 5977442
GENERAL INFORMATION:
APPLICANT: Klessig, Daniel F.
APPLICANT: Zhang Zhuqun
TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
TITLE OF INVENTION: Map kinase and its use for Enhanced Disease Resistance in P
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
ADDRESSER: P. C.
STREET: 1601 Market Street, Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: United States of America
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,593
FILING DATE: April 21, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,805
FILING DATE: October 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: Rutgers 97-0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1544 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE: tobacco
US-08-837-593-1

Query Match	32.0%;	Score 552;	DB 2;	Length 1544;
Best Local Similarity	70.1%;	Pred. No. 4.4e-143;		
Matches 757; Conservative	0;	Mismatches 320;	Indels 3;	Gaps 1;

OY	15	TGTTTTCCTTGGTTTAACTACGCGCGGACAAATATGACAGTTGGATATTTTGGTAA	214
Db	221	TAAATATTCGGCGCGCTTGAGCCACGGTGGACGTTTCATTAATACAAATATTTTGGTAA	280
OY	215	TTTCTTTGAGATCTACTACCAAGTATGCTCTCTCATATTAAGCCATTATGGTGGTGCTTA	274
Db	281	TATATTTGAAGTTACTGCTCAATATATAAGCCTCTCATTTTGGCTATTGGTAAAGTGCTTA	340
OY	275	TGCAATTGTCTGCTCGGTGTTGAATACGCACTGAAATGATGATGGTTCAGTTAAGAAAT	334
Db	341	CGGGATCGTTTGTCTCTCTTGAACCTCGGAGCAATTTGAAGCAATGACGATTAAGAAAT	400
OY	335	CGCAATAGCGTTTATATTTTACATGGATGGCTAGAGAGCTGTCGCGAGATTAACCTCT	394
Db	401	CGCAATATGCTTTTATATACAAAGATGTATGCGCAAGAGACTTTGAGAGAGATCAACCTTCT	460
OY	395	CGCGCAATTTAGACCATGAAATATGTAATTTGGTTTAAAGACGTAATTCCTCCACCTTACG	454
Db	461	TGGCATATGGATCATGATAAAACATTTGTGGATCAGAGATATATATTCACCCACAGAG	520
OY	455	AAGGAGTTTTCATATGTTTACATTTGCTACTGAATCATGATTAAGTATCTTACCAAT	514
Db	521	AGAGGCTTTTAAGATATTTTATATGTGATGAGCTTAAGGATACGTATCTCCATCAAT	580
OY	515	AATTAGATCCAACCCAGGTTTATCAGAGATCACTGTCACTGACTTCATCATGATCACTGCT	574
Db	581	TATTGCGCTAATCAGGGTTTATCTGAGAGACGCTGCAATTTCTTGTATACATCT	640
OY	575	CCGTGGCTAAATATACATATTCGCGAATGTTCTTCAATAGATCTCAACGAGCA	634
Db	641	CCGAGGGTTGAAATACATATCTTCGGAATGTTCTGCAAGGAGCTTGAACCCATGACA	700
OY	635	CCTTTGGTAAATCAATTTGATGCTTAAAGATATGCACTTTGGCTTGGCTAGAGCCAA	694
Db	701	TCTCTGTGAATGCCAATCTGTATTTTAAAGATATGTATTTTGGGCTAGCTCGTGTAC	760
OY	695	CATAGAGACAGAAATATGACGGAAATATGTTTAAACAGATGGTACAGGCGACGAGCT	754
Db	761	TTTCGAAACATGACTTTATGACGGAATATGTTGACAAATGATGGTATCGCCACCTGACT	820
OY	755	TTTGTGTAACCTTCACATTAACACTCTCTCTATAGATGTTTGGTGTGCTGGTGTGATCTT	814
Db	821	GTTCCTTAAATTCGCTGACTACTACTACGAGAAATGACGATATGGTACAGGGTTGCATTTT	880
OY	815	CATGAACTTATGATATGAAACCTTTGTTGGTGAAAGATCATATGATCAATATACG	874
Db	881	CATGGAATATATGACAGAAACCCCTATTTCTCTGTAAAGATCACTACACAGCTGCG	940
OY	875	CTTGTTAACGAGCTTCTGGCAACCCCAACAGAAAGCTGATCTTGGCTTCTTCCAAATGA	934
Db	941	TCTTATATGAGAGTTGATGTGTACTCTTTCAGAGGCTGAAGATGAGATTTT---AAATGA	997
OY	935	AGATGCAAAAGATACATACAGCAATCTCCCAACAATCTCGCCACAGACTTACGAGAAT	994
Db	998	GAAATGCAAAAGATACATTCGCGCAACTCTCTTTTACCGCTGACATCATCTTACCTGAAA	1057
OY	995	TTTTCCTCATGTGAACCATTTGCGCTATTGATCTTGGTCATTAATATGTTGACATTTGATCC	1054
Db	1058	GTTTCCACATGTATACCACTCACTGATTTGCTTTCGAGAAATATGCTGACATTTTGTATCC	1117
OY	1055	TACTAGAAGATTTACAGTTTGAGGACATTTAGATCTCCCTACCTTGCAGAAAGCTCCAGA	1114
Db	1118	TAGAAGAGATTAACATTTGAAGTGCACCTTGACATCTCTTACGTGCACTGCTCCACAGA	1177
OY	1115	TGCAAGTGAAGAACGATCTGCGCTGTTCATTTCTTCTTTGACTTTGACATGACAAGAAAT	1174
Db	1178	TATTATGACAGACCCATTTTGCAATGATCTCTTCTTACTCTTGCACTTTGAAACGATGCGCT	1237

Oy 1175 AGGAGGAACGCCAAATTAAAGCANCATATATCAAGGAGCTTTGTCACTGAATCCCTGATA 1234
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Db 1238 TAGCGAGGAGAACAAGTGAAGAGCTGATTTTCAGGGAGTCGCTTGCAATTAACTCTGATA 1297

RESULT 2

US-08-176-620A-3
; Sequence 3, Application US/08176620A

; GENERAL INFORMATION

APPLICANT: Cobb, Melanie H.

APPLICANT: Nye, Steven

TITLE OF INVENTION: A Family of Map2 Protein Kinases

CORRESPONDENCE ADDRESS:

STREET: 1155 Avenue of the Americas

STATE: New York

COUNTRY: 0
ZTP: 10036

COMPUTER READ
MEDIUM TYPE

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/176,620A
FILING DATE: 02 MAY 2004

CLASSIFICATION: 800
; INTRODUCTION / OBJECTIVE INTRODUCTION
;

NAME: Mistrock, S. Leslie

REFERENCE/DOCKET NUMBER: 6526-123

TELEPHONE: (212) 790-9090

TELEX: 66141 PENNIE

; SEQUENCE CHARACTERISTICS:

TYPE: nucleic acid

TOPOLOGY: unknown

FEATURE: ()

LOCATION: 1..1245

C W070 C/T C C

Query Match	13.38;	Score 233;	DB 1;	Length 140/;
Best Local Similarity	55.28;	Prod NO. 7	38-55.	

Matches	346;	conservative	0;	mismatches	425;	indels	18;	gaps	4;
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258 ATTGCTGCTGCTTATGGAATTGCTGCTCGGTGTTGAATACGGAGCTGAATGAGATG 31

Db 256 ATCGGAGAGCGCCCTACGGCATGGTTGTTCTGCTTATGATAATCTCAACAAAGTTCGA 31.

318 GTTCAGTTAAGAAATCGCGAATGCGTTGATATTACATGGATGCTAAGAGGACTCTC 377

Db 316 GTTGTATCAAGAAATC--AGTCTTTTGAGCACCAGACCTACTGTCAGAGAACCCTG 377

378 CGTGAGATTAGCTCCTCCGCCATTAGACCATGA AATGTAATTGCTTAA GAGACGTC 437

Db 373 AGAGAGATAAAATCCTACTGCGCTTCAGACATGAGACATCATTCGGCATCAATGACATC 431

438 ATTCCTCACCCTTACGAGGAGTTTCTGATGTTACATTGCTACTGAACATCATGGAT 497

Db 433 ATCCGGCACCACCATTCAGCAGATGAAGATCTATATAGTACAGGACCTCATGGAG 493

QY	498	ACGATCCTTACC	AAATTAATTAGATTC	CAACCAAGGTTTATCGAGAGTACTGTCAGTAC	557
Db	493	ACGATCTTTTAC	AGCTCTTGAAGACACAGCA	---CCTGACCAAGATCATATCTGCTAT	549
QY	558	TTGATGATGAG	CTCTCCGTGGCCCTTA	AAATACATACATTCGCGGATATGTTCTTCATAGA	617
Db	550	TTTCTTTATC	AGATCCTGAGAGATT	AAAGTATATCATTTAGCTATATGTTCTGCACCGT	609
QY	618	GATCTCAAA	CCGAGCAACCTTTTGGT	AAATGCGAAATTTGATCTTTAAGATATGTGACTTT	677
Db	610	GACCTCAAG	CCCTTCCAAACCTCCGTCG	AACACACACTTGTGATCTCAATCATCTGTGACTTT	669
QY	678	GGTCTTCG	---TAGGCGCA	MAATAGAGAACGAGAAATA-----TGACGGAATATGTT	725
Db	670	GGCTCTCCG	CTTTGTCAGATCTCCAGAC	CCATGTATCATACAGGTTCTTCTTACAGAGATGTA	729
QY	726	GTAACCGAT	GTGTACAGGGACAGAGCT	TTTGTGAACTCTTCAGATTACACTGCTCT	785
Db	730	GCCACGGT	TGTGTACAGAGCTCC	AGAAATTAATGTTGAATCCAAAGGTTATATCCAAAGTCC	789
QY	786	ATAGATGTT	GGTGTGTGCGGTGGCAT	CTTTCATGGAACCTTATGAATAGAAAACCTTTGTTT	845
Db	790	ATTGATAT	TGTTGGTCTGGGCTGCAT	CTCGGAGAGATGCTATCCAAAGGCTATCTTTC	849
QY	846	GGTGGAAA	GAATATATGATCATCA	ATACGCTGTTTACCGAGCTTCTTGGCACCCCAACA	905
Db	850	CCAGAAAG	ATTACCTTGACCGAGT	ATCATCTCTGGTATTTCTTGATCTCTCACTCA	909
QY	906	GAAGCTAT	CTTGGCTTCCCAAAAT	TGAAGATGCAAAAGATACATCAGGCAATCTCCA	965
Db	910	CAGAGAT	CTGATATGTATTA	TAAATTTAAAAAGCTAGAAACTATTTTGTCTTCTCCCG	969
QY	966	CAACATCT	CGCCAGAGTTAGCAGA	AGTTTTCCCTCATGTGAACCAATTGGCTATTGAT	10259
Db	970	CACAAAAT	ATAAGGTCCGCGTGA	AGACAGTGTTCGCCAAACGTGACTCCAAAGCTGTGAT	10299
QY	1026	CTTGTGAT	TAATAATGTTGACAT	TTCATCTCTACTAGAACATTTACAGTTGAGAGACATTA	10855
Db	1030	TTACTGTAT	TAATAATGTTGACAT	TTAACCTCTCAAGAGGATTTGAAGACAGGCTCTG	10899
QY	1086	GATCATCC	TACCTTCCAAAGCTCC	ACAGATGAGGTGAGGAGCAACGATCTGCCCTTTCCA	11455
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QY	1146	TTCTCTTT	GACTTTGAGCAACA	CAAGGAATAGGAGAACCAATTTAAGACATGATATAT	12055
Db	1150	TTCAAGTT	TACATGAGAGCTG	AGCACTTACCTTAAGGAGACGCTCAAAAGAACTCATTTTT	12099
QY	1206	CAGAGACT	TTTGTCACTGAG	ATCTCTGAATA 1234	
Db	1210	GAAGAGAC	TGCTGATTCAC	GCGCCAGGATA 1238	

RESULT 3
 US-08-463-862-3
 : Sequence 3, Application US/08463862
 : Patent No. 5776751
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Boulton, Teri G. et al.
 : TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
 :
 : NUMBER OF SEQUENCES: 11
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Pennie & Edmonds
 : STREET: 1155 Avenue of the Americas
 : City: New York
 : STATE: New York
 : COUNTRY: U S A
 : ZIP: 10036-2711
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25

	CURRENT APPLICATION DATA:	
/	APPLICATION NUMBER: US/08/463,862	
/	FILING DATE: 05-JUN-1995	
/	CLASSIFICATION: 435	
/	PRIOR APPLICATION DATA:	
/	APPLICATION NUMBER: US 07/701,544	
/	FILING DATE: 16-MAY-1991	
/	ATTORNEY/AGENT INFORMATION:	
/	NAME: Mistock, S. Leslie	
/	REGISTRATION NUMBER: 18,872	
/	REFERENCE/DOCKET NUMBER: 6526-049	
/	TELECOMMUNICATION INFORMATION:	
/	TELEPHONE: 212 790-9090	
/	TELEFAX: 212 869-8864/9741	
/	TELEX: 66141 PENNIE	
/	INFORMATION FOR SEQ ID NO. 3:	
/	SEQUENCE CHARACTERISTICS:	
/	LENGTH: 1467 base pairs	
/	TYPE: nucleic acid	
/	STRANDEDNESS: double	
/	TOPOLOGY: unknown	
/	MOLECULE TYPE: DNA (genomic)	
/	FEATURE:	
/	NAME/KEY: CDS	
/	LOCATION: 1..1245	
/	US-08-463-862-3	
<hr/>		
Query Match	13.5%	Score 233; DB 1: Length 1467;
Best Local Similarity	55.2%;	Pred. No. 7.3e-55;
Matches 546; Conservative	0;	Mismatches 425; Indels 18; Gaps
OY	258 ATTTGTCCTGGCGCTTATAGAAATGTCTGCCTCCGCTTGGAATACGGAGCTGATGATG	317
Db	256 ATCGGAGAAGGGCCCTACGGCATGGTTTGCTTATGATAAATCACAAGATTGCA	315
OY	318 GTTGCAGTTAAGAAAATGCCGATCCGTTTGATTAATTACATGAGATGCTAAGAGACTTC	377
Db	316 GTTGTATCAAAAAATC--AGTCCCTTTGGCACACACACCCTACTGTCAGAGAACCCTG	372
OY	378 CGTGAATTAACCTCCCTCCGCCATTAGACATAGAAAATGTAAATTGGTTAAGACAGCTG	437
Db	373 AGAGGATTAATAATCTTACTGCGCTTACAGCATGAGAACATCATCGGCATCATGATC	432
OY	438 ATTCTCCACCCCTTAGAAGGAGTTTTCTGATGTTTACATTGCTACTGAACTCATGAT	497
Db	433 ATCCGGCACCCACCATTTGAGCAGATGAAGAATGTATATAGTACAGAGCCCTCATGAG	492
OY	498 ACTGATCTTCACCAATATATATGATCCAACCAAGTTTATCAGAGATACGTGACGATG	557
Db	493 ACAGATCTTTTAAACCTCTTGAGACACAGCA---CCTTAGCAATGATATATTCGTCTAT	549
OY	558 TTTCATGTATCAGCTCCCTCCGTGGCCTTAATAATACATACATTCCGCGAATGTTCTCATAGA	617
Db	550 TTTCTTTATCAGATCCTGAGAGATTAAAGTATATACATTACGCTAATGTTCTGCACCGT	609
OY	618 GATCTCAACCGACGACCTTTTGGTAAATGCAAAATTTGATCTTAAGTATGTGACTTT	677
Db	610 GAACCTCAAGCCCTTCAACCTCCTGCTGAACACACACTGHTGATCTCAAGATCTGTGACTTT	669
OY	678 GGTCTTGC---TAGGCCCAAATAGAAAGCAGAATA-----TGACGAATATGTT	725
Db	670 GGCTTGTGCCCGTGTTCAGATCCAGACCATGATCATACAGGGTCTTGTACACAGTATGTA	729
OY	726 GTAACCAAGATGATACAGGGCACCAAGACTTTTGTGAACCTTTCAGATTACACTGCTGCT	785
Db	730 GCCAGCGCTGTGTAAGAGCTCCAGAAAATTATGTGAATTCCAAGGCTTATACCAAGTCC	789
OY	786 ATAGATGTTGGTCTGTGGTGTCACATCTTCATGAGAACTTATGATTAAGAAACCTTTGTT	845
Db	790 ATGTGATTTGGTCTGTGGCTGCTCATCTCGCAGAGATGCTATCCACAGGCTTATCTTC	849
OY	846 GGTGAAAAAGATCATGATCATCAATAATACGCTTGTAAACGAGCTTCCTTGGACCCCACCA	905

Oy	1206	CAGGAGCTTTGTCACTGAATCCTGAATA	1234
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		- - - - -	
Db	1210	G A G A G A C T G C T C G A T T C C A G C C A G G A T A	1238

RESULT 5

Sequence 3, Application US/08455887
Patent No. 5914261
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G. et al.
TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penelope & Edmunds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,887
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,544
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1245
US-08-458-887-3

Query Match	13.5%	Score 233;	DB 2;	Length 1467;
Best Local Similarity	55.2%	Pred. No. 7.3e-55;		
Matches 546; Conservative	0;	Mismatches 425;	Indels 18;	Gaps 4;

QY	318	GTTCCAGTTAAAGAAATCGCGAATGCGCTTTGATATTTATTCATATGATGCTAAAGAGACTCTC	3177
Db	256	ATCGGAGAGGCGGCTCAGCGGATGTTTGTCTTATATATATATCATCAACAAAGTTTGA	3155
QY	258	ATTGGTGGTGGTGGTTATATGAAATATGCTGCTCGGCTTTGAAATCGGAGAGCTGAATGATGATG	3175
Db	256	ATCGGAGAGGCGGCTCAGCGGATGTTTGTCTTATATATATATCATCAACAAAGTTTGA	3155
QY	316	GTTTCCTATCAAGAAATATC -- AGTCCTTTTGTAGACACGACGACCTATCTGCAGAACCCCTG	3172
Db	316	GTTTCCTATCAAGAAATATC -- AGTCCTTTTGTAGACACGACGACCTATCTGCAGAACCCCTG	3172
QY	378	CGTAGAATTAGCTCCCTCCGCAATTTAGACCATATGAAATATTAATGTTTAAAGAGAGCTG	4375
Db	378	CGTAGAATTAGCTCCCTCCGCAATTTAGACCATATGAAATATTAATGTTTAAAGAGAGCTG	4375
QY	373	AGAAAGATAAAAATCTCACTGCGGCTTAGACATGAGAACATCATATCGGCATCAATGACATC	4322
Db	373	AGAAAGATAAAAATCTCACTGCGGCTTAGACATGAGAACATCATATCGGCATCAATGACATC	4322
QY	438	ATTGCTCAACCCCTTACGAAAGGAGATTTTTCGATGTTTACATGCTAGCTAGCAATCATGATGAT	4975
Db	433	ATCCGGGCAACCAACCATTTAGACAGATATAAAGATATATATTTAGTACAGGCACTCATATGGAG	4922
QY	498	ACTGATCTTCCCAATTAATTAGATCCCAAGGTTTATCAGAGATCACTGTCAATAC	5575

Db	493	ACAGATCTCTTCAAGACTCTTGAAGACACAGCA	---	CCTCACCAATGATCATATCTGCAT	549	
Oy	558	TTTCATGATTCAGACCTCCCTCGCTAAATATACATACATTCGCGCAATGTTCTTCATAGA	617			
Db	550	TTTCTTTATCAGATCCTAGAGGATTAAGATATATACATTCAGCAATAGTTCTGCACGGT	609			
Oy	618	GATCTCAAAACGAGCAACCTTTTGGTAAATGCAATTTGTATCTTTAGATATGTACCTT	677			
Db	610	GACCTCAAGCCCTCCACCTCCTGCTGAACACACACTTGTGATCTTCACATCTGTGACCTT	669			
Oy	678	GGCTCTGC	---	TAGCCCAACATAGAGAACGAAATA	-----TGACGGAATATTT	725
Db	670	GGCTTGGCCGCTGTTGCAGATCCAGACCATGATCTATACAGSGTTCTTCAGAGATATGA	729			
Oy	726	GTAACCAAGATGGTACAGGGACACAGAGCTTTTGTGAACCTTTCAGATTACATGCTGCT	785			
Db	730	GCCACGCGCTGGTACAGAGCTCCACAAATATATGTGATTTCCAAAGGGTTATACCAAGTCC	789			
Oy	786	ATAGATGTTTGGTCTGTGGTGTGCATCTTCATGGAACCTTATGAATAGAAACCTTTGTT	845			
Db	790	ATTGATTTTGGTGTGGCTGCATCCGTGCAGAGATGCTATCCACAGGCTCATCTTC	849			
Oy	846	GGTGAAGAAAGATCATGATCATCAATACGCTTGTATTAACCGAGCTCTTGGCACCCACACA	905			
Db	850	CCAGSAAAGCATTACCTTGACAGCTGAATCAATCCTGGGATTTCTTGATCTGCATCA	909			
Oy	906	GAACTGATCTTGGCTCTCCCAAAATGAAAGATGCAAGAGATATCAGGCACCTCCCA	965			
Db	910	CAGSAGATCTGAAATGTATATATAATTTAAAGCTAAMAACATTTCTTCTCCCG	969			
Oy	966	CAACATCTCTGCGACACATTTAGACAAATTTTCCCTCATGTGAACCCATTTGGCTTTGAT	1025			
Db	970	CACAAAATTAAGTGTCCGTGAAACAGTTGTTCACAAACGCTGACTCCAAAGCTGTGAT	1029			
Oy	1026	CTTGCTGATAAATGTTGACATTCGATCCTACTAGAGAAATTAACGTTGAGAGACATTA	1085			
Db	1030	TTACGTAGTAAATTTGACATTTTAACTTAACTTCAAGAGAGATTTGAAGTGAACAGGCTCTG	1089			
Oy	1086	GATCATCTCTCTACTGCAACGCTCCAGATGAGGTGAGTGAACGATCTGGCCCTGTCCA	1145			
Db	1090	GCCACCCGTCCTGAGACAGATTTATACCCAACTGATGAGCCCATGCTGAAACACCA	1149			
Oy	1146	TTTCTCTTGAATTTGAGCAACAAAGAAATAGAGAAGCAAAATTTAAGACATGATAT	1205			
Db	1150	TTCAAGTTTGAACATGAGACTGGACACATTTACTTAAGAGAAAGCTCAAAAGACTATTTT	1209			
Oy	1206	CAGGAAGCTTTGTCACTCAATCTGAATA	1234			
Db	1210	GAAAGACTGCTCGATTTCCAGCCAGAGATA	1238			

RESULT 6

US-08-932-787B-3
: Sequence 3, Application US/08932787B
: Patent No. 6277963
: GENERAL INFORMATION:
: APPLICANT: Boulton et al.
: TITLE OF INVENTION: ANTIBODIES DIRECTED TOWARD EXTRACELLULAR SIGNAL-RELATED
: TITLE OF INVENTION: KINASES
: FILE REFERENCE: REG 430-A-1
: CURRENT APPLICATION NUMBER: US/08/932.787B
: CURRENT FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 08/469,547
: PRIOR FILING DATE: 1995-06-06
: PRIOR APPLICATION NUMBER: 08/178,488
: PRIOR FILING DATE: 1994-01-07
: PRIOR APPLICATION NUMBER: 07/701,544
: PRIOR FILING DATE: 1991-05-16
: PRIOR APPLICATION NUMBER: 07/532,004
: PRIOR FILING DATE: 1990-06-01
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 3.0

Db 670 GGCCTTGCCCGTGTGAGATCCAGACATGATCATACAGSGTCTGTGCAAGATATGA 729
OY 726 GTAACCAAGATGTACAGGCGACAGAGCTTTGTTGAACCTTTCAGATTACACTGCT 785
Db 730 GCCAGCGCTGTGTACAGAGCTCCAGAAATTATGTGAATTCAGAGGTATACCAAGTCC 789
OY 786 ATGATGTTGGTGTGTGGTGTGCATCTCATGSAACTATATAGAAACTTTGTTT 845
Db 790 ATGTGATTTGGTGTGTGGGTGTCATCCGCGAGATGCTATCCAGACAGGCTATCTTC 849
OY 846 GGTGGAAGAATGATGATCATCAATATAGCTTTTAACCGAGCTTGTGGCACCCCAACA 905
Db 850 CCAGAAAGCATTTACTTGACAGCTGAATCATCTCGGTATTTCTTGATCTGCATCA 909
OY 906 GAACTGATCTTGCTCTCTCCAAAATGAGATGCAAAAGATATCATCAGCACTCCCA 965
Db 910 CAGGAAGATCTGAAATTGATATATAATTTAAAGCTAGAACTATTTGCTTCTCCCG 969
OY 966 CAACATCTCGCCAGCAGTTAGCAGAAAGTTTCCCTCATGTGACCCCATTTGCTATTGAT 1025
Db 970 CACAAAAATTAAGTCCGTGTGCAACAGGTTGTTCCAAACGCTGACTCCAAAGCTCTGGAT 1029
OY 1026 CTGTGATAAATGTTGACATTCGATCTACTAGAGAAATTACAGTTGAGGAGACATTA 1085
Db 1030 TTACTGATAAATGTTGACATTTAACCTTCACAGAGGATTTGAAGTTGAACAGCTCTG 1089
OY 1086 GATCATCTCCCTACCTGCAAAAGCTCCAGATGAGGTGACGAACCATCTGCCCTTTCCA 1145
Db 1090 GCCACCCGTCCTGAGCAGATTTATATGACCCAAAGTGTGACCCATTCGCTGAAACACCA 1149
OY 1146 TTCTCCTTTGACTTTGACCAACAGAAATAGAGAAAGCAATTAAGACATGATATAT 1205
Db 1150 TTCAAGTTTGACATGAGACTTGACAGACTTACTTAAGAGAAAGCTCAAGAACTCATTTT 1209
OY 1206 CAGGAAGCTTTGTCTACGTAATCTGAATA 1234
Db 1210 GAAGAGACTGCTGATTCAGATTCAGCCAGAGATA 1238

RESULT 8
US-08-888-818C-3
: Sequence 3, Application US/08888818C
: Patent No. 6303358
: GENERAL INFORMATION:
: APPLICANT: Boulton et al.
: TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
: FILE REFERENCE: REG 430-V-1
: CURRENT APPLICATION NUMBER: US/08/888, 818C
: PRIOR FILING DATE: 1997-07-07
: PRIOR APPLICATION NUMBER: 08/478, 985
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: 08/178, 488
: PRIOR FILING DATE: 1994-01-07
: PRIOR APPLICATION NUMBER: 07/701, 544
: PRIOR FILING DATE: 1991-05-16
: PRIOR APPLICATION NUMBER: 07/532, 004
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 1467
: TYPE: DNA
: ORGANISM: RAT
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(1245)
: OTHER INFORMATION: ERK2 CDNA
US-08-888-818C-3

Query Match 13.5%; Score 233; DB 4; Length 1467;
Best Local Similarity 55.2%; Pred. No. 7.3e-55;
Matches 546; Conservative 0; Mismatches 425; Indels 18; Gaps 4;

OY 258 ATTGCTCGTGTGCTTATGAAATTGTCTGCTGCTGTTGAATACGAGCTGAATGATG 317
Db 256 ATCGAGAGAGGGCGCTACGCGATGGTTGTTCTGCTTATGATTAATCTCAAAAGTCTGA 315
OY 318 GTTGAGTTAAGAAAATGCGGAATGCGTTGATTTATTTACATGATGCTAAGAGAGCTTC 377
Db 316 GTTGCTATCAAGAAATC---AGTCTTTTGGACACAGAGCTACTGCTAGAGAACCTTG 372
OY 378 CGTGAGATTAAAGCTCCCGCATTTAGACATGAAATGTAATGCTTTAAGAGACGTG 437
Db 373 AAGAGATTAATAATCTACTGCGCTTGACAGATGAGAAATCATATGGCATCAATAGACAT 432
OY 438 ATTCTCCACCTTACGAAGGAGTTTCTGATTTTACATTGCTACTGACTATGAT 497
Db 433 ATCCGGGACCAACCATTTGAGCAGATGAAAGATGATATATATGTAACAGACCTCATGGAG 492
OY 498 ACTGATCTTACCAATAATATGATCCAAACCAAGTTTATCAGAGATCACTGCAGTAC 557
Db 493 ACAGATCTTTACAGCTCTTGAAGACAGCA---CTTCAGCAATGATCATATCTGCTAT 549
OY 558 TTGATGATACAGCTCTCCGTCGCTAAATATCATACATTCGCGAATGTTCTGATAGA 617
Db 550 TTTCTTTATCAGATCTCTGAGAGATTTAAAGTATATACATTCAGTAATGTTCTGCACGT 609
OY 618 GATTCGAAACGAGACACTTTTGTAAATGCAATTTGATCTTAAATATGATATGACTTT 677
Db 610 GACCTCAAGCTTTCACACTCTCTGCTGAACACACACTTGTGATCTCAAGCTGTGATCTT 669
OY 678 GGTCTTGC---TAGGCCAAATAGAGAAACGAGATA-----TGACGGAATATGTT 725
Db 670 GGCCTTGCCCGTGTGAGATCCAGACATGATCATACAGGTTCTTGACAGAGATATGA 729
OY 726 GTAACCAAGTGTACAGGCGACAGAGCTTTGTTGAACCTTTCAGATTACACTGCTGCT 785
Db 730 GCCAGCGCTGTGTACAGAGCTCCAGAAATTATGTGAATTTCCAAAGGTTATACCAAGTCC 789
OY 786 ATGATGTTGGTGTGTGGTGTGCATCTTCATGSAAGTAATATAGAAACTTTGTTT 845
Db 790 ATTTGATTTTGTGTGTGGGTGTCATCTCGCAGAGATGCTATCCAGACGGCTATCTTC 849
OY 846 GGTGGAAGAATGATGATCATCAATATAGCTTTTAACCGAGCTTGTGGCACCCCAACA 905
Db 850 CCAGAAAGCATTTACTTGACAGCTGAATCATCTCGGTATTTCTTGATCTGCATCA 909
OY 906 GAACTGATCTTGCTCTCTCCAAAATGAGATGCAAAAGATATCATCAGCACTCCCA 965
Db 910 CAGGAAGATCTGAAATTGATATATAATTTAAAGCTAGAACTATTTGCTTCTCCCG 969
OY 966 CAACATCTCGCCAGCAGTTAGCAGAAAGTTTCCCTCATGTGAAACCATTTGCTATTGAT 1025
Db 970 CACAAAAATTAAGTCCGTGTGCAACAGGTTGTTCCAAACGCTGACTCCAAAGCTCTGGAT 1029
OY 1026 CTGTGATAAATGTTGACATTCGATCTACTAGAGAAATTACAGTTGAGGAGACATTA 1085
Db 1030 TTACTGATAAATGTTGACATTTAACCTTCAGAGAGATTTGAAGTTGAACAGCTCTG 1089
OY 1086 GATCATCTCCCTACCTGCAAAAGCTCCAGATGAGGTGACGAACGATCTGCCCTTTCCA 1145
Db 1090 GCCACCCGTCCTGAGCAGATTTATATGACCCAAAGTGTGACCCATTCGCTGAAACACCA 1149
OY 1146 TTCTCCTTTGACTTTGACCAACAGAAATAGAGAAAGCAATTAAGACATGATATAT 1205
Db 1150 TTCAAGTTTGACATGAGACTTGACAGACTTACTTAAGAGAAAGCTCAAGAACTCATTTT 1209
OY 1206 CAGGAAGCTTTGTCTACGTAATCTGAATA 1234
Db 1210 GAAGAGACTGCTGATTCAGATTCAGCCAGAGATA 1238

RESULT 9
US-08-950-449A-18
: Sequence 18, Application US/08950449A

```

? Patent No. 5955366
? GENERAL INFORMATION:
? APPLICANT: Lee, John C.
? APPLICANT: Adams, Jerry L.
? APPLICANT: Gallagher, Timothy F.
? APPLICANT: Green, David W.
? APPLICANT: Heyes, J. Richard
? APPLICANT: McDonnell, Peter
? APPLICANT: McNulty, Dean E.
? APPLICANT: Strickler, James E.
? APPLICANT: Young, Peter R.
? TITLE OF INVENTION: Drug Binding Protein
? NUMBER OF SEQUENCES: 19
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: SmithKline Beecham Corporation
? STREET: Corporate Intellectual Property/P.O. Box
? STREET: 1539
? CITY: King of Prussia
? STATE: PA
? COUNTRY: USA
? ZIP: 19406-0939
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/950,449A
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/123,175
? FILING DATE: 17-SEP-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Hecht, Elizabeth J.
? REGISTRATION NUMBER: P-41,824
? REFERENCE/DOCKET NUMBER: P50195-1D1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (610) 270-5009
? TELEFAX: (610) 270-5090
? INFORMATION FOR SEQ ID NO: 18:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1100 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? US-08-950-449A-18

Query Match 13.4%; Score 232; DB 2; Length 1100;
Best Local Similarity 56.5%; Pred. No. 1.2e-54;
Matches 496; Conservative 0; Mismatches 370; Indels 12; Gaps 3;

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Db 336 ATGGGGGAGATCTGAACCAATTTGTGAAT---CTCAGAAGCTTTACAGATGACCATGTT 392
Qy 552 CAGTACTTCATGTATGAGCTCCCGGCGCTTAATAATACATATCCGGGAATGCTCT 611
Db 393 CAGTCTTATCTACCAAAATTTCTCGAGGCTTAAGATATATACATAGCTGACATATTT 452
Qy 612 CATAGAGATCTCAACCGAGCAACCTTTGGTAAATCAAAATTTGATCTTAAAGATATGT 671
Db 453 CACAGGGACCTAAACCTAGTAATCTAGTGTGAATGAAGACTGTGAGCGGAATCTCTG 512
Qy 672 GACTTTGGTCTGTCTAGGCCCAATATGAGACAGAAATATGACGGAATATGTTTGAAC 731
Db 513 GATTTGGAGCTGGCTCGCACA-----CAGATGATAAATGAGACGCTGAGCGCACT 566
Qy 732 AGATGTACAGAGGACAGACCTTTGTTGTAAGCTTCTCAGATTCACCTGCTGCTATAGAT 791
Db 567 AGTGTGTACAGAGGCTCTGAGATCATCTGAACTGATGATTTCAACAGCAAGTTGAT 626
Qy 792 GTTTGGTCTGTGGTTCATCTTCATGAACTTATGAAATGAAAACTTTGTTGGTGA 851
Db 627 ATTTGGTCAGTGGGATCATATGCGGAGCTTTGACTGGAAAGACATTTGTTCCGTGT 686
Qy 852 AAAGATCATGATCAATCAATATAGCTTTGTAACGAGAGCTTCTGGCACCACAGAAAGCT 911
Db 687 ACAGACCATATTTAACAGCTTCAGACATTTATGCTGTGACAGAGAACACCCCGCTTAT 746
Qy 912 GATCTTGCTCTCTCCAAATGAAATGAAATGAAAGATACATCAGCAACTCCCAACAT 971
Db 747 CTCATTTAACAGAGATGCCAGGACATGAGCAAGAAATCATATTCAGTCTTTGAGTCAGAT 806
Qy 972 CCTCGCCAGAGATTAGCAGAAATTTCCCTCAGTATGTAACCCATTTGCTATGATCTTGTCT 1031
Db 807 CCGAAGATGAACTTTGGGAATGTAATTTATGTCGCAATCCCGGCTGTGCTGCTG 866
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Qy 1092 CCTTACCTTGCAAGCTCCAGAGATGAGGTGAGCAACC 1129
Db 927 GCTTACTTTGCTGCTAGTACACGATCTGATGATGATTAAC 964

RESULT 10
US-08-950-449A-11
? Sequence 11, Application US/08950449A
? Patent No. 5955366
? GENERAL INFORMATION:
? APPLICANT: Lee, John C.
? APPLICANT: Adams, Jerry L.
? APPLICANT: Gallagher, Timothy F.
? APPLICANT: Green, David W.
? APPLICANT: Heyes, J. Richard
? APPLICANT: McDonnell, Peter
? APPLICANT: McNulty, Dean E.
? APPLICANT: Strickler, James E.
? APPLICANT: Young, Peter R.
? TITLE OF INVENTION: Drug Binding Protein
? NUMBER OF SEQUENCES: 19
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: SmithKline Beecham Corporation
? STREET: Corporate Intellectual Property/P.O. Box
? STREET: 1539
? CITY: King of Prussia
? STATE: PA
? COUNTRY: USA
? ZIP: 19406-0939
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:

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Db 523 CGTGTGGCAGTGAAGACGCTCTCCAGACATTTTCAGTCATTCATTCGCGAAGAAC 582
Qy 375 CTCCTGAGATTAGCTCTCCGCAATTAGACCATGAAATGTATTGGTTAAGAGAC 434
Db 583 TACAGAGAACTCGGCTACTTAACATATGAACATGAAATGTATTGGTCTGTTGAC 642
Qy 435 GTGATT---CCTCCACCTTACGAAGAGTTTCTGATGTTTACATTGCTACAGC 491
Db 643 GTTTTACACCTCGAAGCTCTCTGAGGAATTCATGATGTATCTGTGTCACCATCTC 702
Qy 492 ATGATAGTATCTCTACCAATAATATTAGATCAACCAAGTTTATCAGAGATCACTGT 551
Db 703 ATGGGGGAGATCTGAACAATTTGTGAAT---GTCAAGACTTACAGATACCATGTT 759
Qy 552 CAGTACTTATGATATCAGCTCTCCGCGCTTAAATACATATCATTTCCGCAATTTCTT 611
Db 760 CAGTCCCTTATCTACCAATTTCTCGAGGTCAAGTATATCATTTACGCTGACATTAAT 819
Qy 612 CATAGAGATCTCAACCGAGACCTTTTGTAAATGCAATTTGATCTTAAGATATGT 671
Db 820 CACAGGAGCTTAAACCTAGTATCTAGCTGTGAATGAAGACTGTGACCTGAAGATTCTG 879
Qy 672 GACTTGTGCTTGTAGCGCAAAACATAGAAACGAAATATGACGGAATATGTTTAACC 731
Db 880 GATTTTGACCTGGCTCGGCACA-----CAGATGATGAATGACAGCTAGCTGGCCACT 933
Qy 732 AGATGTACAGGCGACACAGACCTTTGTTGAACCTTCAGATTACAGTGGCTATAGAT 791
Db 934 AGGTGTACAGGCGCTCGAGCATCATGCTGAACCTGATGATTCACACGACAGCTGTAT 993
Qy 792 GTTTGTGCTGTGGTTGATCTCTCATGAACTTATGAAATGAAACCTTTGTTGGTGA 851
Db 994 ATTTGTAGTGGGATGTGATTAATGCGCGAGCTGTGACCTGGAGAATGTTGTTCTGCT 1053
Qy 852 AAAGATCATGATCAATCAATAGCTTTGTTAAACCGAGCTTCTTGGCACCACCAAGAGCT 911
Db 1054 ACAGACCATATTAACACACTTCAGCAGATTAATGCTGTGACAGGAACACCCCCCTTAT 1113
Qy 912 GATCTGGCTTCTCCAAATGAAGATCCAAAGAGATCAATCAGGCAACTCCACACAT 971
Db 1114 CTCATTAACAGAGATCCCAAGCATGAGCAAGAACTATATTCACCTTTGATCAGATG 1173
Qy 972 CCTGCGCCAGGATGAGCAAGTTTCCCTCATGTGAAACCATTTGGCTATTGATGTC 1031
Db 1174 CCGAAGATGAACCTTGGCAATGTATTATTGGTCCAAATCCCTGGCTGACACTGGC 1233
Qy 1032 GATAAATGTGACATTCGATCTACTAGAAATTTACAGTTGAGAGACATTAGATCAT 1091
Db 1234 GAGAAGATGCTTGTATGTGACTCAGATTAAGAAATTTACAGCGGCCCAAGCCTTGCACAT 1293
Qy 1092 CCTTACCTTGCAGAACTCCAGATGACAGTGAACACC 1129
Db 1294 GCTTACTTGTCTCAGTACAGATCCTGATGATGAACC 1331

RESULT 13
US-08-605-002A-11
Sequence 11, Application US/08605002A
Patent No. 5871934

GENERAL INFORMATION:
APPLICANT: Lee, John C.
APPLICANT: Adams, Jerry L.
APPLICANT: Gallagher, Timothy F.
APPLICANT: Green, David W.
APPLICANT: Livi, George P.
APPLICANT: McDonnell, Peter
APPLICANT: McLaughlin, Megan M.
APPLICANT: McNulty, Dean E.
APPLICANT: Strickler, James E.
TITLE OF INVENTION: Drug Binding Protein
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithline Beecham Corporation

STREET: Corporate Intellectual Property/P.O. Box
STREET: 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,002A
FILING DATE: 15-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Hecht, Elizabeth J.
REGISTRATION NUMBER: P-41,824
REFERENCE/DOCKET NUMBER: P50195-1 U.S. (PCT)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5009
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Monocyte
FEATURE:
NAME/KEY: CDS
LOCATION: 379..1461
US-08-605-002A-11
Query Match 13.4%; Score 232; DB 2; Length 3813;
Best Local Similarity 56.5%; Pred. No. 2.2e-54;
Matches 496; Conservative 0; Mismatches 370; Indels 12; Gaps 3;
Qy 255 CCTATTGTCGTGGTCTTATGAAATGCTCTGCGTGAATACAGAGCTGATGAG 314
Db 463 CCAGTGGGCTCTGGGCGCTATGCTGTGTGCTGCTTTGACACAAAACGGGGTTA 522
Qy 315 ATGGTTGAGTAAAGAAATCGGAATGCGTGTGATTTTACATGATGCTAAGAGCT 374
Db 523 CGTGTGGCAGTGAAGAGCTCTCCAGACCATTTACGTCATTCATTCAGGAAAGAAC 582
Qy 375 CTCCTGAGATTAGCTCTCCGCAATTAGACCATGAAATGTATTGGTTAAGAGAC 434
Db 583 TACAGAGAACTCGGCTACTTAACATATGAACATGAAATGTATTGGTCTGTTGAC 642
Qy 435 GTGATT---CCTCCACCTTACGAAGAGTTTCTGATGTTTACATTGCTACTGAATC 491
Db 643 GTTTTACACCTCGAAGCTCTCTGAGGAATTCATGATGTATCTGTGTCACCATCTC 702
Qy 492 ATGATAGTATCTCTACCAATAATATTAGATCAACCAAGTTTATCAGAGATCACTGT 551
Db 703 ATGGGGGAGATCTGAACAATTTGTGAAT---GTCAAGACTTACAGATACCATGTT 759
Qy 552 CAGTACTTATGATATCAGCTCTCCGCGCTTAAATACATATCATTTCCGCAATTTCTT 611
Db 760 CAGTTCCTTATCTACCAATTTCTCGAGGTCAAGGTATATCATTCAGCTGACATTAAT 819
Qy 612 CATAGAGATCTCAACCGAGACCTTTTGGTAAATGCAATTTGATCTTAAGATATGT 671
Db 820 CACAGGAGCTTAAACCTAGTATCTAGCTGGAATGAAGACTGTGACCTGAAGATTCTG 879
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Db 880 GATTGTGACTGGCTGGCACA-----CAGATGATGAATGACAGGCTAGTGGCCACT 933
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Db 934 AGGTGTACAGAGGCTCTGATGATCATGCTGACCTGATGCTTTCACACAGAGTTGAT 993
QY 792 GTTGTGCTGTGGTGTGATCTTCATGAACTTATGAAATAGAAAACCTTTGTTGGTGA 851
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Db 994 ATTTGGTCAGTGGGATCATTAATGCGGAGCTGTTGACTGGAAACAATGTTCTCGGT 1053
QY 852 AAAGATGATGATGATCAAAATACGCTGTTAAACGAGCTCTTGGACCCCAAGAAAGCT 911
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Db 1054 ACAGACCATATTAACAGCTTACAGACATTTATGCGCTGACAGAAACACCCCGCTTAT 1113
QY 912 GATCTGGCTCTCTCAAAATGAAGATGAAGATACATCAGCAACTCCACAAACAT 971
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Db 1114 CTCAATTAACAGGATGCCAAGCATGAGGCAAGAAACTATATTCAGTCTTTGACACAGTG 1173
QY 972 CCTGCGCAGCATTTAGCAGAAATTTCCCTCATGTGAACCCATGGCTATGATCTGTGC 1031
  || || || || || || || || || || || || || || || || || || || || ||
Db 1174 CCGAAGATGAACCTTGGCAATGATTTATTTGTCGCAATCCCTGGCTGTGACTGTGCTG 1233
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  || || || || || || || || || || || || || || || || || || || || ||
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RESULT 14
US-08-943-353-11
; Sequence 11, Application US/08943353
; Patent No. 6361773
; GENERAL INFORMATION:
; APPLICANT: Lee, John C.
; APPLICANT: Adams, Jerry L.
; APPLICANT: Gallagher, Timothy F.
; APPLICANT: Green, David W.
; APPLICANT: Heys, J. Richard
; APPLICANT: McDonnell, Peter
; APPLICANT: McNulty, Dean E.
; APPLICANT: Strickler, James R.
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: Drug Binding Protein
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Intellectual Property/ P.O. Box
; STREET: 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,353
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/468,902
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/250,975
; FILING DATE: 31-MAY-1994
; APPLICATION NUMBER: US 08/123,175
; FILING DATE: 17-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jervis, Herbert H.

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; REGISTRATION NUMBER: 31,171
; REFERENCE/DOCKET NUMBER: P50195-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5019
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: Monocyte
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 379..1461
; US-08-943-353-11

Query Match 13.4%; Score 232; DB 4; Length 3813;
Best Local Similarity 56.5%; Pred. No. 2,2e-54;
Matches 496; Conservative 0; Mismatches 370; Indels 12; Gaps 3;

QY 255 CCTATTGCTGCTGCTTATGAAATGCTCGCTGCTGTTGAATACGAGCTGAATGAG 314
  || || || || || || || || || || || || || || || || || || || || ||
Db 463 CCACTGGGCTCTGGCGCTATGCTGTGTCTGCTCTTGTGACACAAAAGGGGTTA 522
QY 315 ATGTGCACTTAAGAAATCGCAATGCGTTGATATTACATGATGCTTAAGAGACT 374
  || || || || || || || || || || || || || || || || || || || || ||
Db 523 CGTGTGCAGAGGAAGAGCTCTCCAGACCAATTCAGTCATCATTCAGGAAAGAAC 582
QY 375 CTCGTGAGATTAAGTCCTCCGCCATTTAGACCATGAATGAATGTTGTTAAGAGC 434
  || || || || || || || || || || || || || || || || || || || || ||
Db 583 TACAGAACTGCGGTTACTTAACATATGAAACATGAATGATGATGTTGTTGAC 642
QY 435 GTGAT---CCTCCACCCTTAGAAGGAGTTTCTGATGTTTCAATGCTAGTGAAC 491
  || || || || || || || || || || || || || || || || || || || || ||
Db 643 GTTTTACCTGCAAGGTCTCTGGAGAAATTAATGATGTATGTTGATGACCATCTC 702
QY 492 ATGATATCTGATCTTCAACCAATTAATTAATGATCAACCAAGTTTATAGAGATCATGT 551
  || || || || || || || || || || || || || || || || || || || || ||
Db 703 ATGGGGCAGATCTGAACACATGTGAAT---GTGAGAACTTAACAGATGACCATGTT 759
QY 552 CAGTACTTCAATGATGATGCTGCTCCGCTGCTTAATATACATTCGCGAATGTTCTT 611
  || || || || || || || || || || || || || || || || || || || || ||
Db 760 CAGTTCCTTATCTACCAATTTCTCCGAGTCTTAAGTATATACATTCAGCTGACATATTT 819
QY 612 CATAGATCTCAACCGAGCAACCTTTTGTGAATGCAAAATGATGATCTTAAGATATGT 671
  || || || || || || || || || || || || || || || || || || || || ||
Db 820 CACAGGACCTAAACCTAGTAATCTAGCTGAATGAAGACTGTGAGTGAACATTTCTG 879
QY 672 GACTTGTCTTCTAGGCCAAGATAGACAGCAATATGACGGAATATGTTGTAAAC 731
  || || || || || || || || || || || || || || || || || || || || ||
Db 880 GATTGTGACTGGCTCGCACA-----CAGATGATGAATGACAGCTACGTGGCCACT 933
QY 732 AGATGTACAGGAGCAGAGCTTTGTTGAACCTTCAGATCTACATGCTGCTATGAT 791
  || || || || || || || || || || || || || || || || || || || || ||
Db 934 AGGTGTACAGGAGCTCTGATGATCATGCTGACCTGATGCTTTCACACAGAGTTGAT 993
QY 792 GTTGTGCTGTGGTGTGATCTTCATGAACTTATGAAATAGAAAACCTTTGTTGGTGA 851
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 994 ATTTGGTCAGTGGGATCATTAATGCGGAGCTGTTGACTGGAAACAATGTTCTCGGT 1053
QY 852 AAAGATGATGATGATCAAAATACGCTTGTAAACGAGCTCTTGGACCCCAAGAAAGCT 911
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1054 ACAGACCATATTAACAGCTTACAGACATTTATGCGCTGACAGAAACACCCCGCTTAT 1113
QY 912 GATCTGGCTCTCTCAAAATGAAGATGAAGATACATCAGCAACTCCACAAACAT 971
  || || || || || || || || || || || || || || || || || || || || ||
Db 1114 CTCAATTAACAGGATGCCAAGCATGAGGCAAGAAACTATATTCAGTCTTTGACTGATG 1173

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[illegible]

```

RESULT 15
PCT-US94-10529-11
Sequence 11, Application PC/TUS9410529
GENERAL INFORMATION:
APPLICANT: Lee, John C.
APPLICANT: Adams, Jerry L.
APPLICANT: Gallagher, Timothy F.
APPLICANT: Green, David W.
APPLICANT: Heys, J. Richard
APPLICANT: McDonnell, Peter
APPLICANT: McNulty, Dean E.
APPLICANT: Strickler, James E.
APPLICANT: Young, Peter R.
TITLE OF INVENTION: Drug Binding Protein
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property/ P.O. Box
STREET: 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10529
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,175
FILING DATE: 17-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jervls, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: P50195-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Monocyte
FEATURE:
NAME/KEY: CDS
LOCATION: 379..1461
PCT-US94-10529-11

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Query Match	13.48;	Score 232;	DB 5;	Length 3813;
Best Local Similarity	56.58;	Pred. NO. 2.2e-54;		
Matches 496;	Conservative 0;	Mismatches 370;	Indels 12;	Gaps 3;

OY	255	CCATATGGCTCGTGGCTGTATATGCAATATGTCTGCTGGTGTGATATCCGAGCTGATATGAG	314
Db	463	CCAGTGGGCGCTGGCGCCCTATAGGCTCTGTGTGTGTGCTCTTTTGACACAAAACGGGGTTA	522
OY	315	ATGTTGTCAGTTAAAGAAAATCGCGAATGCGTTTGATATTTACATGATGATGCTAAAGAGACT	374
Db	523	CGTGGGACAGTGAAGAAAGCTCTCCAGACACTTTTTCACATCATCATTCATTCATCGAAAAAGACC	582
OY	375	CTCCGTGAGATTAAAGCTCTCCGCAATTTAGACCATGAAGAAAATGTATTTGTTAAGACAC	434
Db	583	TACAGAGAACTGGCGGTACTTAAACATATGAAACATGAAAAATGTGATTTGGTGTGGTGAAC	642
OY	435	GTGATT---CCCTCCACCCTTACGAGAGGAGATTTTCTGATGATTTTACATTTGCTACTGACTC	491
Db	643	GTTTTACACCTGCAAGSTGCTCGAGAGAAATTCATATGATGTGATCTGTGACCATCTGC	702
OY	492	ATGATACTGATCTTCCACCAATATTTAGATCCACACCAAGTTTATCAGAGATCTACTGT	551
Db	703	ATGGGGGAGATGTGAAACCAACATTTGTAAT---GTCAACAGCTTACAAATATACCATGTT	759
OY	552	CAGTACTTCATGTTACAGCTCTCCGCGGCTTAAATACATACATATCCGCAATCTGTT	611
Db	760	CAGTTCCTTATCTACCAAAATTTCTCCGAGGCTTAAAGTATATACATTACAGCTACATTAAT	819
OY	612	CATAGAGATCTCAACCCGAGCAACTTTTGGTAAATGCAAAATTTGATCTTAAATATGT	671
Db	820	CACAGGGACCTTAAACCTACTAATCTAGCTGTAAAGAAAGACTGTGAGCTGAAGAAATTCG	879
OY	672	GACTTTGGTCTTGTATAGGCCCAACATATAGAAACGAAATATACGGAATATGTATAC	731
Db	880	GATTTTGGACTGTGCTCGGACACA-----CAGATGATGAAATGACAGGCTACGTCGCCACT	933
OY	732	AGATGTGACAGGGCACCGACAGACTTTTGTGTAACCTTTCAGATTACACTGCTCTATAGAT	791
Db	934	AGGTGTGTACAGGGCTCTGTAGATCATGTCTGAATGATGATGCATTTACACACGACAGTGTAT	993
OY	792	GTTTGTGTCTGCGGTTGCACTTTCATGAGAACTTATGATATGAAAACTTTGTTGGTGTGA	851
Db	994	ATTGGTGACAGGGATCATCAATATATGGCCGACGCTGTTACGTGAAGAACATTTGTTCTCGGT	1053
OY	852	AAAGATCATGTACATTCAAATATACGCTTGTATACGAGACTTCTTGACACCCCAACAACT	911
Db	1054	ACAAGCCATATTAACGACGCTTACGACGATTTATGCGTCTACAGGAACACCCCGCGCTTAT	1113
OY	912	GATCTTGGCTCTCCCAAAATGAAGATGCAAAGAGATACATGAGCACTCCCCACACAT	971
Db	1114	CTCATTTAAACAGAGATGCCACMACCCATAGAGCAAGAACTATATTCAGCTTTGACTCAGATG	1173
OY	972	CCCTGGCAGAGATTAGCAGAAAGTTTTCCTCATATGTAACCCATTTGGCTATATGATCTGTC	1031
Db	1174	CCGAAGATGAACCTTGGGCAATGTATTTATTGTTGGCCAAATCCCTGGCTGTGCACTTGTCTG	1233
OY	1032	GATAAAAATTTGATCATCTCGATCTCTAGTAAGAAATTTAGTTAGGAAAGCATTTAGATCAT	1091
Db	1234	GAGAAAGATGCTGTATGTAGCATCAGATTAAGAGAAATTTACAGCGGCGCAAGCCCTTCACAT	1293
OY	1092	CCCTACTCTGCAAAAGCTCCACGATGACAGGTGACGAACC	1129
Db	1294	GCTTACTTTGTGCTAGTACACGATCTCTGATGATGAACAC	1331

Search completed: May 19, 2003, 23:01:20
Job time : 118 secs

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;
;      FEATURE:
;      NAME/KEY:      CDS
;      LOCATION:      379..1461
;
PCT-US94-10529-11

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GenCore version 5.1.5
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OM protein - protein search, using sw model

Run on: May 19, 2003, 22:59:26 ; Search time 63 Seconds

(without alignments)
793.158 Million cell updates/sec

Title: US-09-623-034-2

Perfect score: 1987

Sequence: 1 MADANMGAGGGGPPDPFVSVL.....EEQIKDMITQELSLNPEYA 375

Scoring table:

BIOSDM62
Gapop 10.0 , Gapept 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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3: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
4: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
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22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
24: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1987	100.0	375	18	AAW15512
2	1764.5	88.8	423	18	AAW15513
3	1523	76.6	398	22	AAAB48048
4	1500	75.5	398	22	AAAB48047
5	1498.5	75.4	395	21	AAAG31653
6	1493	75.1	374	22	AAAB48046
7	1490	75.0	374	21	AAAG34157
8	1488.5	74.9	382	21	AAAG31654
9	1487.5	74.9	366	21	AAAG31655
10	1482	74.6	393	19	AAW61252

11	1365	68.7	330	21	AAAG34158
12	1349.5	67.9	372	21	AAAG3123
13	1349.5	67.9	372	22	AAAB48044
14	1344.5	67.7	376	21	AAAG04672
15	1334	67.1	358	21	AAAG31124
16	1309	65.9	371	21	AAAG45420
17	1290	64.9	316	21	AAAG34159
18	1244.5	62.6	373	21	AAAG30672
19	1219	61.3	372	21	AAAG42613
20	1219	61.3	406	21	AAAG42612
21	1217	61.2	372	21	AAAG06702
22	1217	61.2	379	21	AAAG06701
23	1204.5	60.6	354	21	AAAG30978
24	1134	57.1	311	23	AAAG5837
25	1117	56.2	367	21	AAAG4793
26	1117	56.2	368	21	AAAG35746
27	1117	56.2	368	21	AAAG44792
28	1117	56.2	370	21	AAAG35745
29	1117	56.2	370	21	AAAG44791
30	1117	56.2	370	22	AAAB48045
31	1117	56.2	434	21	AAAG35744
32	1087	54.7	366	21	AAAG4681
33	1087	54.7	367	21	AAAG44680
34	1087	54.7	369	21	AAAG4679
35	1086	54.7	369	22	AAAB48043
36	1078	54.3	370	21	AAAG31572
37	1073	54.0	370	21	AAV77976
38	1069	53.8	376	21	AAAG53018
39	1067.5	53.7	350	21	AAAG31573
40	1061	53.4	366	21	AAAG29650
41	1061	53.4	368	21	AAAG29649
42	1061	53.4	422	21	AAAG29648
43	1058.5	53.3	356	21	AAAG3019
44	1048	52.7	280	21	AAAG04673
45	1048	52.7	338	21	AAAG31574

ALIGNMENTS

```
RESULT 1
ID AAW15512
AAW15512 standard; protein: 375 AA.
AC AAW15512;
DT 04-JUN-1997 (first entry)
DE MAP kinase #1.
KW Mitogen activated protein kinase; MAP; infectious specific protein;
  plant; jasmonate acid.
OS Synthetic.
PN JP09065881-A.
PD 11-MAR-1997.
PF 29-AUG-1995; 95JP-0220935.
PR 29-AUG-1995; 95JP-0220935.
(NORQ ) NORINSUISANSO NNGYO SEIBUTSU SHIGEN.
WPI: 1997-220416/20.
N-PSDB: AAT60349.
PT Wound-stress inducible MAP kinase - used to regulate the synthesis
  of jasmonate acid
PS Claim 2; Page 13-14; 21pp; Japanese.
XX
```

CC AAM1512 and AAM1513 represent the mitogen activated protein (MAP)
 CC kinases of the invention. This sequence contains the T-E-Y sequence, in
 CC which the threonine and tyrosine residues are phosphorylated to activate
 CC the protein at residues 201-203. The MAP kinase and its gene can be used
 CC to regulate the synthesis of jasmonic acid and the synthesis of a group
 CC of infectious specific proteins. By introducing the MAP kinase gene into
 CC a plant, thereby inducing expression of the mRNA for MAP kinase (or its
 CC antisense RNA), the synthesis of jasmonic acid and a group of infectious
 CC specific proteins can be regulated in the plant.

XX Sequence 375 AA;

Query Match 100.0%; Score 1987; DB 18; Length 375;
 Best Local Similarity 100.0%; Pred. No. 4.7e-198;

Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADANMGAGGQPPDPSPVLTGGQYVQFDLFGNFFETTKYRPPIMPIGAGYICSV 60
 DB 1 MADANMGAGGQPPDPSPVLTGGQYVQFDLFGNFFETTKYRPPIMPIGAGYICSV 60
 QY 61 LNFELNEMVAVKKIYANAFDIYMDAKRTLRKILRHLDHENVIGLRDVIPLRREFSDV 120
 DB 61 LNFELNEMVAVKKIYANAFDIYMDAKRTLRKILRHLDHENVIGLRDVIPLRREFSDV 120
 QY 121 YIATELMDTDLHQIIRSNQGISSEDCQYFMYQLRGKLYHSANVLRDLKPSMLYAN 180
 DB 121 YIATELMDTDLHQIIRSNQGISSEDCQYFMYQLRGKLYHSANVLRDLKPSMLYAN 180
 QY 181 CDLKICFGLARPIENENMTEYVYTRMYRAPPELLNSSDVTALIDVWSVCIFMELN 240
 DB 181 CDLKICFGLARPIENENMTEYVYTRMYRAPPELLNSSDVTALIDVWSVCIFMELN 240
 QY 241 KPLFGKHVHQIRLITLLETGPTLADLGLQNEADAKRYIRQLPQHPROQLAEVPHVNP 300
 DB 241 KPLFGKHVHQIRLITLLETGPTLADLGLQNEADAKRYIRQLPQHPROQLAEVPHVNP 300
 QY 301 LAIDLVRKMLTFDPTTRKITYEALDHPYLAKLHDAGDEPTCPVPSFDFEQQGIGEBQIK 360
 DB 301 LAIDLVRKMLTFDPTTRKITYEALDHPYLAKLHDAGDEPTCPVPSFDFEQQGIGEBQIK 360
 QY 361 DMITQEALSLNPEYA 375
 DB 361 DMITQEALSLNPEYA 375

RESULT 2

AAM1513
 ID AAM1513 standard; protein; 423 AA.

XX AAM1513;

XX 04-JUN-1997 (first entry)

XX MAP kinase #2.

XX Mitogen activated protein kinase; MAP; infectious specific protein;

XX plant; jasmonic acid.

XX Synthetic.

XX JP09065881-A.

XX 11-MAR-1997.

XX 29-AUG-1995; 95JP-0220935.

XX 29-AUG-1995; 95JP-0220935.

XX (NORO) NORINSUISANSNO NOGYO SEIBUTSU SHIGEN.

XX WPI; 1997-220416/20.

XX DR N-PADB; AAT60350.

PT Wound-stress inducible MAP kinase - used to regulate the synthesis
 PT of jasmonic acid

XX Claim 3; Page 16-17; 21pp; Japanese.

CC AAM1512 and AAM1513 represent the mitogen activated protein (MAP)
 CC kinases of the invention. This sequence contains the T-E-Y sequence, in
 CC which the threonine and tyrosine residues are phosphorylated to activate
 CC the protein at residues 249-251. The MAP kinase and its gene can be used
 CC to regulate the synthesis of jasmonic acid and the synthesis of a group
 CC of infectious specific proteins. By introducing the MAP kinase gene into
 CC a plant, thereby inducing expression of the mRNA for MAP kinase (or its
 CC antisense RNA), the synthesis of jasmonic acid and a group of infectious
 CC specific proteins can be regulated in the plant.

XX Sequence 423 AA;

Query Match 88.8%; Score 1764.5; DB 18; Length 423;
 Best Local Similarity 97.7%; Pred. No. 8.3e-175;

Matches 336; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 32 FGNFFETTKYRPPIMPIGAGYICSVLTTELNEMVAVKKIYANAFDIYMDAKRTLR 91
 DB 83 FGNFFETTKYRPPIMPIGAGYICSVLTTELNEMVAVKKIYANAFDIYMDAKRTLR 91
 QY 92 KLRHLDHENVIGLRDVIPLRREFSDVYIATELMDTDLHQIIRSNQGISSEDCQYFM 151
 DB 143 KLRHLDHENVIGLRDVIPLRREFSDVYIATELMDTDLHQIIRSNQGISSEDCQYFM 151
 QY 152 QLRLGKLYHSANVLRDLKPSMLYANCDLKICDGLARPIENENMTEYVYTRMYRA 211
 DB 200 QLRLGKLYHSANVLRDLKPSMLYANCDLKICDGLARPIENENMTEYVYTRMYRA 211
 QY 212 PELLNSSDVTALIDVWSVCIFMELNRRKPLFGKHVHQIRLITLLETGPTLADLGL 271
 DB 260 PELLNSSDVTALIDVWSVCIFMELNRRKPLFGKHVHQIRLITLLETGPTLADLGL 319
 QY 272 QNEADAKRYIRQLPQHPROQLAEVPHVNPPLAIDLVDKMLTFDPTTRKITYEALDHPYLAK 331
 DB 320 QNEADAKRYIRQLPQHPROQLAEVPHVNPPLAIDLVDKMLTFDPTTRKITYEALDHPYLAK 379
 QY 332 LHDAGDEPTCPVPSFDFEQQGIGEBQIKDMITQEALSLNPEYA 375
 DB 380 LHDAGDEPTCPVPSFDFEQQGIGEBQIKDMITQEALSLNPEYA 423

RESULT 3

AAB48048
 ID AAB48048 standard; protein; 398 AA.

XX AAB48048;

XX 19-MAR-2001 (first entry)

XX Signal transduction protein.

XX Zea mays; maize; signal transduction protein; phytohormone; ethylene;

XX auxin; cytokinin; gibberellin; immunogen.

XX Zea mays.

XX WO200070059-A2.

XX 23-NOV-2000.

XX 28-APR-2000; 2000WO-US11687.

XX 14-MAY-1999; 99US-0134292.

XX 08-JUL-1999; 99US-0142996.

XX (PIONER) PIONEER HI-BRED INT INC.

XX Helentjaris TG;

XX WPI: 2001-031929/04.
DR N-PSDB: AAC84265.
XX
XX New signal transduction nucleic acids and encoded proteins useful for
PT regulating phytohormone expression, including ethylene, auxins,
PT cytokinins and gibberellin, to provide control of plant response to
PT environmental stresses -
XX
XX Claim 13; Page 97; 126pp; English.
XX
XX The invention provides Zea mays signal transduction proteins and encoding
CC nucleotide sequences. The nucleic acids are useful for regulating
CC expression of phytohormones, including ethylene, auxins, cytokinins,
CC and gibberellin, to effect developmental changes in plants and provide
CC control of plant response to environmental stresses. They may also be
CC used as probes or amplification primers in the detection, quantitation or
CC isolation of gene transcripts, for detecting mutations in the gene, for
CC monitoring upregulation of expression or changes in enzyme activity in
CC screening assays of compounds, for detection of any number of allelic
CC variants, or for site-directed mutagenesis in eukaryotic cells. They may
CC further be used for recombinant expression of their encoded polypeptides,
CC as immunogens in the preparation or screening of antibodies, and in sense
CC or antisense suppression of genes in a host cell, tissue or plant. The
CC proteins may be used in assays for enzyme agonists or antagonists, as
CC immunogens or antigens to obtain antibodies specifically immunoreactive
CC with the proteins. The present sequence represents a signal transduction
CC protein of the invention.
XX
XX Sequence 398 AA;
SQ
Query Match 76.6%; Score 1523; DB 22; Length 398;
Best Local Similarity 72.9%; Pred. No. 1.1e-149;
Matches 283; Conservative 44; Mismatches 45; Indels 16; Gaps 3;
QY 1 MADANMAGGCGGFDPF-----SVLHGGQYVQFDIFGNFETTTKYPPI 46
DB 12 MTDAGLG-CGGQPPPPQPPAGGAGMMENIHATLSHGGRFIOYNIFGVNFEVTSKYPPI 70
QY 47 MPIGRGAYGIVCSVLTENLKNVAVKKTANAFDIYMDAKRTLREIKLRHLDHENYIGLR 106
DB 71 LPIGKAGVIGVCSALNSETAEQVAIKTANAFDNKIDAKRTLREIKLRHMDHENYIVAIR 130
QY 107 DVIPPLLRERSDYIAELMDTDJHOITIRSNQGLSEBHCQYFMVOLLRLGLKYTHSAVYL 166
DB 131 DIIPPLLEARNDYIAELMDTDJHOITIRSNQGLSEBHCQYFLYOLLRLGLKYTHSAVYL 190
QY 167 HRDLKPSNLLVANCDLKCDFGLARPIENENMTEYVTRVYRAPPELLNSSDXTAID 226
DB 191 HRDLKPSNLLVANCDLKCDFGLARTSETDFMEYVTRVYRAPPELLNSSSETTAID 250
QY 227 VWSVGCIFMELMNRKPLDFGKDVHQIRLLTLLTGPTEADLGLQNEDEAKRYIRQLDPQH 286
DB 251 VWSVGCIFMELMNRKPLDFGRDHYHQIRLLTLLTGPTEADLGLQNEDEAKRYIRQLDPQH 309
QY 287 PROQLAEVFPVNPPLAIDLVMKLTEDPTRTVTEALDHPYLAQLHAGDEPITCPVPFS 346
DB 310 ARQSEPFEPFVNPPLAIDLVMKLTEDPTRTVTEALHAPYLAQLHAGDEPITCPVPFS 369
QY 347 FDFEQQGIGEBQIKDMIVQEALESUNPEY 374
DB 370 FDFEQQHALSEQMKDLIVQEALESUNPEY 397
RESULT 4
AAB48047
ID AAB48047 standard; protein: 398 AA.
XX
AC AAB48047;
XX
XX 19-MAR-2001 (first entry)
XX Signal transduction protein.

XX Zea mays; maize; signal transduction protein; phytohormone; ethylene;
KM auxin; cytokinin; gibberellin; immunogen.
XX
XX Zea mays.
XX OS
XX WO200070059-A2.
XX
XX 23-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US11687.
XX
XX 14-MAY-1999; 99US-0134292.
PR 08-JUL-1999; 99US-0142996.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Helentjaris TG;
DR WPI: 2001-031929/04.
DR N-PSDB: AAC84262.
XX
XX New signal transduction nucleic acids and encoded proteins useful for
PT regulating phytohormone expression, including ethylene, auxins,
PT cytokinins and gibberellin, to provide control of plant response to
PT environmental stresses -
XX
XX Claim 13; Page 94; 126pp; English.
XX
XX The invention provides Zea mays signal transduction proteins and encoding
CC nucleotide sequences. The nucleic acids are useful for regulating
CC expression of phytohormones, including ethylene, auxins, cytokinins,
CC and gibberellin, to effect developmental changes in plants and provide
CC control of plant response to environmental stresses. They may also be
CC used as probes or amplification primers in the detection, quantitation or
CC isolation of gene transcripts, for detecting mutations in the gene, for
CC monitoring upregulation of expression or changes in enzyme activity in
CC screening assays of compounds, for detection of any number of allelic
CC variants, or for site-directed mutagenesis in eukaryotic cells. They may
CC further be used for recombinant expression of their encoded polypeptides,
CC as immunogens in the preparation or screening of antibodies, and in sense
CC or antisense suppression of genes in a host cell, tissue or plant. The
CC proteins may be used in assays for enzyme agonists or antagonists, as
CC immunogens or antigens to obtain antibodies specifically immunoreactive
CC with the proteins. The present sequence represents a signal transduction
CC protein of the invention.
XX
XX Sequence 398 AA;
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Query Match 75.5%; Score 1500; DB 22; Length 398;
Best Local Similarity 71.9%; Pred. No. 2.7e-147;
Matches 279; Conservative 45; Mismatches 48; Indels 16; Gaps 3;
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DB 12 MSEAGAG-CGGQPPQPPPLPVGGGYMLDNICATLSHGGRFIOYNIFGVNFEVTSKYPPI 70
QY 47 MPIGRGAYGIVCSVLTENLKNVAVKKTANAFDIYMDAKRTLREIKLRHLDHENYIGLR 106
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QY 107 DVIPPLLRERSDYIAELMDTDJHOITIRSNQGLSEBHCQYFMVOLLRLGLKYTHSAVYL 166
DB 131 GIIPPAQRAFDYIAELMDTDJHOITIRSNQGLSEBHCQYFLYOLLRLGLKYTHSAVYL 190
QY 167 HRDLKPSNLLVANCDLKCDFGLARPIENENMTEYVTRVYRAPPELLNSSDXTAID 226
DB 191 HRDLKPSNLLVANCDLKCDFGLARTSETDFMEYVTRVYRAPPELLNSSSETTAID 250
QY 227 VWSVGCIFMELMNRKPLDFGKDVHQIRLLTLLTGPTEADLGLQNEDEAKRYIRQLDPQH 286
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QY 287 PROOLAEVFFHVNPLAIDLVNKMILTFDPTRITVEALDHPYLAKHDAGDEPICPVFFS 346
Db 310 PROSLPEKFPVHVOPLAIDLVNKMILTFDPTRITVEGALAHPLASLHDIDSDPCSMFFS 369
QY 347 FDFEOGIGGEIOIKMDIYOEALSLNPEX 374
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AC AAG31653;
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 38048.
XX
KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Best Local Similarity	71.4%	Pred. No. 3.8e-147		
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db	10	ADTEMTAPGCGPAPSPOMGIEINIFATLSHGREFIOYNFGNLEFETATKPPIMI	69	

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QY 350 EQOGIGEOIKDMITQOALSINPEY 374
Db 369 ENHALSEEQMKELLYREALAFNPEY 393
RESULT 6
AAB48046
ID AAB48046 standard; protein; 374 AA.
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XX AAB48046;
XX AC
XX 19-MAR-2001 (first entry)
XX DT
XX DE
XX Signal transduction protein.
XX
XX Zea mays; maize; signal transduction protein; phytohormone; ethylene;
KW auxin; cytokinin; gibberellin; immunogen.
OS
XX Zea mays.
XX
XX WO200070059-A2.
XX PN
XX 23-NOV-2000.
XX PD
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XX 28-APR-2000; 2000WO-US11687.
XX PF
XX 14-MAY-1999; 99US-0134292.
XX PR 08-JUL-1999; 99US-0142966.
XX
XX (PION-) PIONEER HI-BRED INT. INC.
XX PA
XX Helentjaris TG;
XX PI
XX WPI: 2001-031929/04.
XX DR N-PSDB: AAC64259.
XX
XX New signal transduction nucleic acids and encoded proteins useful for
PT regulating phytohormone expression, including ethylene, auxins,
PT cytokinins and gibberellin, to provide control of plant response to
XX environmental stresses -
XX
PS Claim 13; Page 91; 126pp; English.
XX
XX The invention provides Zea mays signal transduction proteins and encoding
CC nucleotide sequences. The nucleic acids are useful for regulating
CC expression of phytohormones, including ethylene, auxins, cytokinins,
CC and gibberellin, to effect developmental changes in plants and provide
CC control of plant response to environmental stresses. They may also be
CC used as probes or amplification primers in the detection, quantitation or
CC isolation of gene transcripts, for detecting mutations in the gene, for
CC monitoring upregulation of expression or changes in enzyme activity in
CC screening assays of compounds, for detection of any number of allelic

KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
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PR	25-OCT-1999;	9905-01614065;
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PR	26-OCT-1999;	9905-01613601;
PR	26-OCT-1999;	9905-01613611;
PR	28-OCT-1999;	9905-01619220;
PR	28-OCT-1999;	9905-01619692;
PR	28-OCT-1999;	9905-01619933;
PR	29-OCT-1999;	9905-01621442;

Query Match	74.9%	Score 1488.5;	DB 21;	Length 382;
Best Local Similarity	72.3%;	Pred. No. 4e146;		
Matches 272;	Conservative 49;	Mismatches 42;	Indels 13;	Gaps 2;

OY	11	GQP-----DEPSVLTHGGQYVEDIFGNFELTTTKRPIIMPIMGGAIVC	58
Db	6	GGFPAAAPSPOMPIENIPATLSHGGRFIQYNIGFNFEVTAKKKPPIMDIGGAAGIYC	65
OY	59	SULNTELEMYAVKIKANAEDFYDADARTLREIKLLHLDHENYICLRDVIPPLREFS	118
Db	66	SAMSETRSESVAITKIANAEONKIDAKRTTRELKLLHHMHENVALRIDIIPLLRAFN	125
OY	119	DVYTATELTDLQIIRISNGSLSEDCCQFYMYOLLGLKYIHSAHYLHDLKPSNLTVN	178
Db	126	DVYTATELTMDTDNQIIRSNALSEEHCQFYLYILGLKTYIHSAHYLHDLKPSNILLN	185
OY	179	ANCDLKICDFGLARPNIENEMETVEYVTWYRAPELLNSSDYTAALDWASVCIFMEELM	238
Db	186	ANCDLKICDFGLARVSSEDMETVEYVTWYRAPELLNSSDYTAALDWASVCIFMEELM	245
OY	239	NRKPLFGSKDHVHOIRLLTELGTPTADLCFLONEDAKKRIQLPQHPOOLAEPVPHV	298
Db	246	DRKLPLFGSDHVOIRLLTLMELICTGSPSEEELEFL-NENAKKRYIQRLPPYPROSTIDKFPTY	304
OY	299	NPLALIDLVDKMLTFDPNRRTIVEBALDHPYALKLHDAGDEPICPVPSPFEOOGIGEEO	358
Db	305	HPLALIDLEKKULTDPNRRRTIVDALAHAYLNLSLHDIISDEPECTIPPNFOFHMAHLSSEO	364

Qy	359	IKDMTYOEALSLNPEY	374	
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Db	365	MKEIlyREALAFNPEY	380	
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ID	AAg31655			
XX	AAg31655	standard; Protein: 366	AA.	
AC	AAg31655;			
XX				
XX	17-OCT-2000	(first entry)		
DE	XX	Arabidopsis thaliana protein fragment SEQ ID NO: 38050.		
XX				
KW	XX	Protein identification; signal transduction pathway; metabolic pathway;		
KM	XX	hybridisation assay; genetic mapping; gene expression control; promoter;		
KW	XX	termination sequence.		
OS	XX	Arabidopsis thaliana.		
PN	XX	Ep1033405-A2.		
PD	XX	06-SEP-2000.		
PF	XX	25-FEB-2000; 2000EP-0301439.		
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PR	03-JUN-1999;	99US-0137502.		
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PR	07-JUN-1999;	99US-0137724.		
PR	08-JUN-1999;	99US-0138094.		
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PR	17-JUN-1999;	99US-0139492.		

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PR 02-AUG-1999; 99US-0146388.
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PR 21-OCT-1999; 99US-0160815.

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PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
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PR	29-OCT-1999;	99US-0162142.
PR	29-OCT-1999;	99US-0162143.

Query Match 68.78; Score 1365; DB 21; Length 330;

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Matches 243; Conservative 52; Mismatches 33; Indels 0; Gaps 0;

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Qy	47	MPREGVGVCSVLNTELNMVAVKKIAAFLDYDAKKTAEIKLRLLDHENNYIGLR	106
Db	1	MPJORGAVGVCSVMNSETKEVAAIKIAAFOHMDAKKTEELREIKLRLLDHENNYIGLR	60
Qy	107	DVLPPLRREESDYVYIAETELMDTDLHQIIRNSOGLEDSDHQCYPMYQLLRLLKTYHSANVL	166
Db	61	DVLPPEAPQAFNDVYISTELMDTDLHHIIRNSQELSEHSQYFLYQLLRLLKTYHSANVI	120
Qy	167	HRDLKPSNLLVNMNCOLKICDFFGLARRINENENKTEVYVYRWYRAPPELLNSSDYTAID	226
Db	121	HRDLKPSNLLVNMNCOLKICDFFGLARRSSSDMMTEVYVYRWYRAPPELLNSTDYSAID	180
Qy	227	VWSVGCIFMELMNKKPLFGKGRVHQIRLLTELLGTPTAEADLFQLENDKAKRYIRLOLPOH	286
Db	181	VWSVGCIFMELINQPLFPGRDHMQKRLITVEYIGPTDDELGINEDAKRYMRHLPQF	240
Qy	287	PROGLAEFVHPVPLAIDLWDKMLTPRPTRRIVEALDHPYLAKLHDAGDEPICYPPFS	346
Db	241	PRRFVYSLFRPMQVADLILERMILTPRPLORIVVEALEHPLYERLHDVADDEPICYDPPFS	300
Qy	347	PDFEQGIGGEQIKMDIYQEALSINPEY	374
Db	301	PDFEQQLTEDQKQKLFENATIELNPF	328

RESULT	12
ID	AAG33123
AA	AAG33123 standard; Protein; 372 AA.
AC	AAG33123;
DT	18-OCT-2000 (first entry)
DE	Zea mays protein fragment SEQ ID NO: 40087.
XX	
XX	
KM	Protein identification: signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
XX	termination sequence; corn.
XX	
OS	Zea mays subsp. mays.
XX	
PN	EPI033405-A2.
PD	
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
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PR	23-MAR-1999; 9905-0125788.
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PR	29-MAR-1999; 9905-0126785.
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PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

	Query Match	67.9%	Score 1349.5;	DB: 21;	Length 372;		
	Best Local Similarity	64.7%	Pred. No. 1.le-131;				
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Oy	3 DANMAGGGQFPDPFSVLTGHGGOYOFDIFGNFFETTRKYPPIIMPIGRGAYGVCSVLN 62	:	:	:	:		
Db	2 DSSGGGGGAQ---IKGMATHGGRVLYLANYGNLFVESSKTAPRIPIRIGGATGIYCAAVN 58	:	:	:	:		
Oy	63 TELNEMVAVKRIANAEDIDYMDAKRTLREIKLRHLHDHENYVIGLDVYIPPLRLREFSDVYI 122	::	:	:	:		
Db	59 SOSGEVAIVKKYGNAFDNHIDAKRTLREIKLRHMDHENILAKDVIRPPTRENFNVDYI 118	::	:	:	:		
Oy	123 ATELMDTDLHQIRSNOSGISSEHCQYFMQLRGKYITHSANVLRHDLKPSNLVYAND 182		:	:	:		
Db	119 VTELMDDTLHQIVRSNOPTLTDHCQFLYQLLRGLKYHSANILHRDLKPSNFLFVAND 178		:	:	:		
Oy	183 LKICDFGLARPIENENMTVEYVTWYRAPDELLNSSDTAAIDWVSVCIMELNRKP 242		:	:	:		
Db	179 LKIADFGIARTISELDIMYEYTVTKMYRAPPELLLNCSOYTAAIDWVSVCIIIGEIVTRQP 238		:	:	:		
Oy	243 LFEGDHVHQRLLTELLESTPEADLGFIQNEDAKRYINQLPQHPRQOLAEPVPHYNPLA 302		:	:	:		
Db	239 LFPGRDYIQOQLKLITELLIGSPDDASIGFLRSNNAKRYMKQLQPPRODRFLFRNNSPGA 298		:	:	:		
Oy	303 IDLVKNMLTFPDRTKITVEALDHPYLAKLHADGPETCPVPFSPFEQGSGEEDIKDM 362		:	:	:		
Db	299 VDLEKRMVLVDFDSKRITVDVALHHPLYLASLHEINDEPTCPAPFSFDEQSFSTEAIKEL 358		:	:	:		
Oy	363 IYQEALSLNPE 373	:	:	:	:		
Db	359 IMRESLAENP 369	:	:	:	:		
RESULT 13							
AC	AAB48044	ID	AAB48044 standard; protein; 372 AA.				
XX	AAB48044;						
XX	19-MAR-2001 (first entry)						
XX	Signal transduction protein.						
XX	Zea mays; maize; signal transduction protein; phytohormone; ethylene;						
XX	auxin; cytokinin; gibberellin; immunogen.						

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Query Match 67.7%; Score 1344.5; DB 21; Length 376;
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Matches 243; Conservative 63; Mismatches 65; Indels 1; Gaps 1;

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QY 62 NTELNEMVAVYKINANADIWDARKRTLREIKLLRHLDHENYIGLRDVIIPPLRREFSDYV 121
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PR 28-OCT-1999; 99US-0161992.
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PR 29-OCT-1999; 99US-0162142.

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Qy	141	LSEDHCQYFMYQLRGJTKYINSANVLHRDLKPSMILVANACDLKICDPCGAPRIENEM	200
Db	123	LTDHCGYFELQQLRGJTKYVNSAIIHRDLKPSMILFANODLKIAPFGIARITTSIEDLM	182
Qy	201	TEYVYTRMYRAPPELLNSSDYTAIIDWVSVCIMELMANKRPFLGCGDHYHQIRLITELL	260
Db	183	TEYVYTRMYRAPPELLNCSQYTAIIDWVSVCIIIGETVYTRPRLPEGRDYYIOQKLTIELI	242
Qy	261	GTPTEADJGFLQNNDAKRYIKQLRQHPROOLAEEVFPVNPFLAIDLVKMLTDPTRRTYV	320
Db	243	GSPDASISGFLRSQNAKRYMQLQRPQRODFRLFRMNSGCAVDLLERMVLVFDPSRRTYV	302
Qy	321	EEALDHPILAKLHAGDEPFCIPVPFSDFFBQSIGEBQIKDMITYOELSLNPE	373
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Job time : 65 secs
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GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2003, 20:53:56 ; Search time 4374 Seconds

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Title: US-09-623-034-1

Perfect score: 1725

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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5	738.4	42.8	1495	8	AF149424	AF149424 Ipomoea b
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12	577.2	33.5	1597	8	NTP45NTP4	X83880 N.tabacum m
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DEFINITION Tobacco cDNA encoding a wound induced protein kinase.
ACCESSION E12716
VERSION E12716.1 GI:3251548
KEYWORDS JP 1997065881-A/1.
SOURCE Nicotiana tabacum.
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE
AUTHORS Ohashi, Y. and Seo, S.
TITLE WOUND STRESS INDUCING MAP KINASE AND ITS GENE

JOURNAL Patent: JP 1997065881-A 1.11-MAR-1997;
 NORIN SUISANSTO NOGIO SEIBOTSU SHIGEN KENKYUSHO

COMMENT OS Nicotiana tabacum
 PN JP 1997065881-A/1
 PD 11-MAR-1997
 PF 29-AUG-1995 JP 1995220935
 PI OHASHI YUKO, SEO SHIGEMI
 PC C12N15/09,C07K14/415,C12N5/10,C12N9/12,C12P7/40,C12P7/42, PC
 C12P7/62,
 PC C12P19/44,C12P21/02,(C12P7/40,C12R1:91),(C12P7/42,C12R1:91),
 PC C12P7/62,
 PC C12R1:91),(C12P19/44,C12R1:91),(C12P21/02,C12R1:91); CC
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 FT after infection
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BASE COUNT 469 a 361 c 326 g 569 t

ORIGIN

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Dd	961	TCCCAACAATCTCTGCGCACAGTTAGACAGAACTTTCCCTCATGTGAAACCCATGGCTA	1020
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Dd	1021	TTGAGTCTTGTCGATAAATATGTACAAATGTGATCCTCTCTGAAGAATTTACAGTTAGAGAG	1080
Qy	1081	CATTAGATCATCCCTTACCTTGCAAAGCTCCACGATGACAGGTAGAGCAACGATCTGCCCCG	1140
Dd	1081	CATTAGATCATCCCTTACCTTGCAAAGCTCCACGATGACAGGTAGAGCAACGATCTGCCCCG	1140
Qy	1141	TTCCATTCTCTTGAATCTTGGACACAAAGAAATAGAGAAAGCAAAATTAAGACATGAG	1200
Dd	1141	TTCCATTCTCTTGAATCTTGGACACAAAGAAATAGAGAAAGCAAAATTAAGACATGAG	1200
Qy	1201	TATATCAGAGAAGCTTTGTCACTGAATCTGCAATGCTTAAACATPAGAGAAATCAATTC	1260
Dd	1201	TATATCAGAGAAGCTTTGTCACTGAATCTGCAATGCTTAAACATPAGAGAAATCAATTC	1260
Qy	1261	TTCTTCTCTCTGTCTCCCTTTGATCTGAGATCTACCTTCTCTACTGTGAGATTTCTTCC	1320
Dd	1261	TTCTTCTCTCTGTCTCCCTTTGATCTGAGATCTACCTTCTCTACTGTGAGATTTCTTCC	1320
Qy	1321	TCGAGACGAGCACTCAATTTTTCTCACTGCTAGCTCTTGCAGCAACTGTGAATGT	1380
Dd	1321	TCGAGACGAGCACTCAATTTTTCTCACTGCTAGCTCTTGCAGCAACTGTGAATGT	1380
Qy	1381	AAGGACGCTTCAATGTGACAGCCATCATATATCTTTTTATTTTTATTTTATTAACG	1440
Dd	1381	AAGGACGCTTCAATGTGACAGCCATCATATATCTTTTTATTTTTATTTTATTAACG	1440
Qy	1441	TGCTGTCTGAGCTAGCTTGTGGGACCTTGATTATTTCAATGTGAATTTGCTACCTCCCG	1500
Dd	1441	TGCTGTCTGAGCTAGCTTGTGGGACCTTGATTATTTCAATGTGAATTTGCTACCTCCCG	1500
Qy	1501	CAGACACAACATTTATCTCCCACTCATTTCTATGATTTGATCTTGTGTGTATTC	1560
Dd	1501	CAGACACAACATTTATATCTCCCACTCATTTCTATGATTTGATCTTGTGTGTATTC	1560
Qy	1561	AGCTAAACCAATATATGACAGGTTCTCTCAACAATCATAGACATCATATGACAGATTT	1620
Dd	1561	AGCTAAACCAATATATGACAGGTTCTCTCAACAATCATAGACATCATATGACAGATTT	1620

QY	1621	CAAGTTTCCTTTTCCAACTTATCTTCTTCAATTCATGACTCTTCACTGAACTTC	1680
DB	1621	CAAGTTTCCTTTTCCAACTTATCTTCTTCAATTCATGACTCTTCACTGAACTTC	1680
QY	1681	TTCCTTCGATGATATATCAACAAAGAGCAAGGACTTGCGTATA	1725
DB	1681	TTCCTTCGATGATATATCAACAAAGAGCAAGGACTTGCGTATA	1725
RESULT 2			
LOCUS	TOBWIPK	1725 bp	MRNA
DEFINITION	TOBACCO mRNA for WIPK, complete cds.	linear	PLN 12-FEB-1999
ACCESSION	D61377		
VERSION	D61377.1	GI:1136297	
KEYWORDS	WIPK.		
SOURCE	Nicotiana tabacum cDNA to mRNA, clone WIPK.		
ORGANISM	Nicotiana tabacum		
REFERENCE	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.		
AUTHORS	Seo, S., Okamoto, M., Seto, H., Ishizuka, K., Sano, H. and Ohashi, Y.		
TITLE	Tobacco MAP kinase: a possible mediator in wound signal transduction pathways		
JOURNAL	Science 270 (5244), 1988-1992 (1995)		
REFERENCE	96123271		
AUTHORS	2 (bases 1 to 1725)		
JOURNAL	Ohashi, Y.		
REFERENCE	Unpublished		
AUTHORS	3 (bases 1 to 1725)		
TITLE	Ohashi, Y.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (26-JUN-1995) Yoko Ohashi, National Institute of Agrobiological Resources, Department of Molecular Biology; Kannonndai 2-1-2, Tsukuba, Ibaraki, Japan		
AUTHORS	(E-mail: yohashies.abr@affrc.go.jp., Tel: 0298-38-7440, Fax: 0298-38-7408)		
FEATURES	Location/Qualifiers		
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	114..1241		
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BASE COUNT	469 a 361 c 326 g 569 t		
ORIGIN			
Query Match	100.0%;	Score 1725;	DB 8; Length 1725;
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Matches 1725;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
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QY	61	TAGGACATATTTTCTTTCTTGACCTAGATTAAGAGCTGAATTAATTCATGCGTG	120
DB	61	TAGGACATATTTTCTTTCTTGACCTAGATTAAGAGCTGAATTAATTCATGCGTG	120
QY	121	ATGCAATATGAGGTCGCGGTGAGGTCAATTCCTGATTTTCCCTTTCGGCTTTAACTCAG	180
DB	121	ATGCAATATGAGGTCGCGGTGAGGTCAATTCCTGATTTTCCCTTTCGGCTTTAACTCAG	180

D	b	121	ATGCAATATGGGTGCGCGGTGGAGGTCGAATTCCTCCGATTTTCTTCCTGGTTTAATCTCACG	180
O	y	181	GGGCAAAATATGTACAGTTTGATTTTGGTAAATTTCTTTAGATCACTACCAAGTATC	240
D	b	181	GGGCAAAATATGTACAGTTTGATTTTGGTAAATTTCTTTAGATCACTACCAAGTATC	240
O	y	241	GTTCCTCTATTTATGCTTATTTGGTCGTGGTCTTATATGAATTTGTCTGCTGGTGTGAATA	300
D	b	241	GTTCCTCTATTTATGCTTATTTGGTCGTGGTCTTATATGAATTTGTCTGCTGGTGTGAATA	300
O	y	301	CGGAGCTGAATAGATAGTTGGAGTTAAACAAATGCGCAATCGTTGATATTTACATAG	360
D	b	301	CGGAGCTGAATAGATAGTTGGAGTTAAACAAATGCGCAATCGTTGATATTTACATAG	360
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D	b	361	ATGCTTAAAGAGACTCCCTGAGATTAAAGCTCCCTCGCATTTAGACATGAAGAAATGTAA	420
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D	b	421	TTGGTTTAAAGACGTGATTTCTCCACCCCTTACGAAGGGAGTTTCTGATGTTTACATTTG	480
O	y	481	CTACTGACTCATGATACTGATCTTTCACCAATAATTTAGATCCAAACGAAGTTTATCG	540
D	b	481	CTACTGACTCATGATACTGATCTTTCACCAATAATTTAGATCCAAACGAAGTTTATCG	540
O	y	541	AGGATCACTGTAGTACTTCATGATATACGCTCCTCGTGCCCTAAAAATCATACATTTCCG	600
D	b	541	AGGATCACTGTAGTACTTCATGATATACGCTCCTCGTGCCCTAAAAATCATACATTTCCG	600
O	y	601	CGAATGTTCTTCATAGAGATCTCAAAACGAGAACCTTTTGGTAAATGCAATTTGTATC	660
D	b	601	CGAATGTTCTTCATAGAGATCTCAAAACGAGAACCTTTTGGTAAATGCAATTTGTATC	660
O	y	661	TTAAGATATGTACTTTGGTCTTCTGCTAGGCCAAACATATAGAACGAGATATAGCGGAT	720
D	b	661	TTAAGATATGTACTTTGGTCTTCTGCTAGGCCAAACATATAGAACGAGATATAGCGGAT	720
O	y	721	ATGTTGTAAACAGATAGTGTACAGGGCAACCGAGACTTTTGTGAAGCTTCAGATTAACAGT	780
D	b	721	ATGTTGTAAACAGATAGTGTACAGGGCAACCGAGACTTTTGTGAAGCTTCAGATTAACAGT	780
O	y	781	CTGCTATAGATGTGGTCTGTGCGGTTGCATCTTATGGAATAGAAAACTT	840
D	b	781	CTGCTATAGATGTGGTCTGTGCGGTTGCATCTTATGGAATAGAAAACTT	840
O	y	841	TGTTTGTGTGAAAAATCATATGTAATCAATTAACGCTTGTAAACGAGCTTCTTGACACC	900
D	b	841	TGTTTGTGTGAAAAATCATATGTAATCAATTAACGCTTGTAAACGAGCTTCTTGACACC	900
O	y	901	CAACGAAACCTGATCTTGCTCTCCCTCCAAATAAGAAAGATGCATCACTAGAGCAAC	960
D	b	901	CAACGAAACCTGATCTTGCTCTCCCTCCAAATAAGAAAGATGCATCACTAGAGCAAC	960
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D	b	961	TCCCAACAACATCTCGCCAGCAGATTAGCAGAAAGTTTCCCTCATGTGAACCCATTGGCTA	1020
O	y	1021	TTGATCTTGTGCATTAATAATGTTGACATTTGATCTCTACTAGAAGAAATTAACGTTGAGAG	1080
D	b	1021	TTGATCTTGTGCATTAATAATGTTGACATTTGATCTCTACTAGAAGAAATTAACGTTGAGAG	1080
O	y	1081	CATTGATATATCCCTTACCTTGGAAAGCTCCACGATGCAAGGTGACGAACCGATCTCCCTG	1140
D	b	1081	CATTGATATATCCCTTACCTTGGAAAGCTCCACGATGCAAGGTGACGAACCGATCTCCCTG	1140
O	y	1141	TTCCCATTTCTCTTGTGACTTTGAGCAACAAGAAATAGAGAAAGCAAAATTAAGGACATGA	1200
D	b	1141	TTCCCATTTCTCTTGTGACTTTGAGCAACAAGAAATAGAGAAAGCAAAATTAAGGACATGA	1200
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D	b	1201	TATATCAGAGACTTTGTCACTGAAATCCTGAAATATGCTTTAAACATATAGGAATCAATTC	1260

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 DB 1441 TCGTGTGAGCTAGCTGTGGGACCTGTGATTTTATTTATTTATTTATTTATTTATTC 1500
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 QY 1681 TTGCTGTGANTGATTAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1725
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RESULT 3

LOCUS E12717 1786 bp DNA linear PAT 27-APR-1998
 DEFINITION Tobacco cDNA encoding a wound induced protein kinase.
 ACCESSION E12717.1 GI:3251549
 VERSION JP 1997065881-A/2.
 KEYWORDS Nicotiana tabacum.
 SOURCE Nicotiana tabacum
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; eunasterids I; Solanales; Solanaceae; Nicotiana.
 1 (bases 1 to 1786)
 Ohashi, Y. and Seo, S.
 WOUND STRESS INDUCING MAP KINASE AND ITS GENE
 Patent: JP 1997065881-A 2 11-MAR-1997;
 NORIN SUIANSYO NOGYO SEIBUTSU SHIGEN KENKYUSHO
 OS Nicotiana tabacum
 PN JP 1997065881-A/2
 PD 11-MAR-1997
 PE 29-AUG-1995 JP 1995220935
 PI OHASHI YUKO, SEO SHIGEMI
 PC C12N15/09, C07K14/415, C12N5/10, C12N9/12, C12P7/40, C12P7/42, PC
 C12P7/62.
 PC C12P19/44, C12P21/02, (C12P7/40, C12R1:91), (C12P7/42, C12R1:91),
 PC (C12P7/62,
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 strandedness: Double;
 CC topology: Linear;
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 ORIGIN

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 Best Local Similarity 99.0%; Pred. No. 5.3e-300;
 Matches 1342; Conservative 0; Mismatches 5; Indels 9; Gaps 1;

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Query	241	GTCTCTCTATTATGCTATTTGCTGGTGGCTTATGAAATGTCTGCTGGTGTGAATA	300			
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Db	ATGTGAAGAGGAGCCTCCGCCAGATTAAGCTTCTTCGCCATTTAGACCATGAAAATGTCA	430
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QY	ATGTGTACACAGATGGTACAGGACACAGAGCTTTTGTGAACCTTCATATACATG	780
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Db	AAGCATATGAGCTTTGGCTGTGCTGATTCATTCATGAGCACTATGAATAGAAAACCTT	850
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FEATURES	source
LOCUS	AF149424
DEFINITION	Ipomoea batatas MAP kinase mRNA, complete cds.
ACCESSION	AF149424
VERSION	AF149424.1 GI:5007037
KEYWORDS	
SOURCE	Ipomoea batatas.
ORGANISM	Ipomoea batatas; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterides I; Solanales; Convolvulaceae; Ipomoea.
REFERENCE	To, K.Y., Suen, D.F. and Chen, S.C.G. Cloning of A Sweet Potato Leaf cDNA (Accession No. AF149424) Encoding Mitogen-Activated Protein Kinase. (PCR99-135)
AUTHORS	Plant Physiol. 121 (1), 312 (1999)
TITLE	2 (bases 1 to 1495)
JOURNAL	To, K.Y., Suen, D.F. and Chen, S.C.G. Direct Submission
REFERENCE	Submitted (10-MAY-1999) Institute of Botany, Academia Sinica, Taipei 11529, Taiwan, Republic of China
AUTHORS	Location/Qualifiers
JOURNAL	1. .1495

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ORIGIN
Query Match      42.8%; Score 738.4; DB 8; Length 1495;
Best Local Similarity 79.2%; Pred. No.3.8e-163;
Matches 890; Conservative 0; Mismatches 231; Indels 3; Gaps 1;
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QY 816 ATTAGAATTTATGAGAAACCTTTGTTGGTGAAGAAAGATCATGTCATCAATATACAGC 875
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QY	876	TTGTTAAACCGAGCTTCTTGACACCCCAACAGAGCTGATCTTGCGTTCTCTCCAAATGAA	935
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QY	936	GATGCAAGAGATACATCAGCGCACTCCACAACTCCTCGGCACAGTATACAGAAATG	995
Db	882	AATGCAAGAGTATATAGCGCACTTCCACTACGTCCACGCCAGCAGTTAGCAAAATGCT	941
QY	996	TTCCCTCATGTGAACCCATTGGCTATTTGATCTTTGATTAATAATGTTGCATTCGATCT	1055
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QY	1056	ACTAGAGAAATTTACAGTTGAGGAGACATTAGATCATCTCCCTACCTTGCAAAAGCTCCACGAT	1115
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Db	1062	AAATCTGATGAACCCATATGCCCCGTTCCATTAC---TGATTTGAGAGAAACAAACCTAT	1118
QY	1176	GGAGAGAGCAAAATTAAGACATGATATATCAGAGAGCTTGCTCACTGATTCCTAAATAT	1235
Db	1119	GGAGAGAGCAAAATTAAGACATGATTTACAGAGAGGACAGCTGCAATGATATCAGAGATAT	1178
QY	1236	GCTTAACATTAAGAGAAATCAATTTCTTCTCTCGTTGCCCT	1279
Db	1179	GCATTAACAAGAGGCGACTACCAATTTCTCCCTTTCTCTCTCCCT	1222

RESULT 6			
LOCUS	MSMK4		
DEFINITION	MSMK4	1695 bp	linear
ACCESSION	X82270		
VERSION	X82270.1		
KEYWORDS	MMK4 gene; protein kinase.		
SOURCE	Medicago sativa.		
ORGANISM	Medicago sativa		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.		
REFERENCE	1 (bases 1 to 1695)		
AUTHORS	Jonak,C.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-OCT-1994) C. Jonak, Inst Microbiol. & Genetics, Vienna Biocenter, Dr. Bohr Gasse 9, 1030 Wien, AUSTRIA		
REFERENCE	2 (bases 1 to 1695)		
AUTHORS	Jonak,C., Kiegehl,S., Ligterink,W., Barker,P.J., Huskisson,N.S. and Hilt,H.		
TITLE	Stress signaling in plants: a mitogen-activated protein kinase pathway is activated by cold and drought		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 93 (20), 11274-11279 (1996)		
MEDLINE	97008170		
PubMed	8653346		
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Db	1160	ATGATGATGCCGATGACACCTATCTCATGAGACCGCATTCCTCATTTGATGTGAGCAACAGC	1219
Oy	1171	GAAATGAGGAAGAGCAAAATTAAGACATGATATATATACAGAGCTTTGTCACTGATCTCGT	1230
Db	1220	ATTTCGATGAGAACAAATTAAGAGATGATATACAGGAGGACGATTAACACTCATCTCGT	1279
Oy	1231	AATATGCTTAA	1242
Db	1280	AGTATGCTTAA	1291
RESULT 7			
LOCUS	AF153061	1643 bp	mRNA
DEFINITION	Pisum sativum MAP kinase 3 (mapk3)	linear	PLN 11-DEC-2000
ACCESSION	AF153061		complete cds.
VERSION	AF153061.1	GI:8132286	
KEYWORDS			
SOURCE	Pisum sativum.		
ORGANISM	Pisum sativum.		
REFERENCE	1 (bases 1 to 1643)		
AUTHORS	Marcote,M.J. and Carbonell,J.		
TITLE	Transient expression of a pea MAP kinase gene induced by gibberellic acid and 6-benzyladenine in unpollinated pea ovaries		
JOURNAL	Plant Mol. Biol. 44 (2), 177-186 (2000)		
PUBMED	21003323		
REFERENCE	2 (bases 1 to 1643)		
AUTHORS	Marcote,M.J. and Carbonell,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-MAY-1999) Biologia del Desarrollo, Instituto de Biologia Molecular y Celular de Plantas (UPV-CSIC), Camino de Vera 14, Valencia 46022, Spain		
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ORIGIN			
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Oy	211	GTAATTTCTTTGAGATCACTACCAAGATGTCGTCCTATTATAGCTATTTGTCGTG	270

Db	149	GTATTCCTTTGGAAGTACTGCTTAAGTATTCGTCTCCATCATAGCCATTTGGTCGGCGC	208
Oy	271	CTTATGGAATTTGCTGCTCGGTGTTAAATACGAGCTGATGAGATGGTTGCAGTTAAGA	330
Db	209	CTTACGGAATCGTTTGTTCCTCTCTTGAACACGAGACGAATGATGGTTCTGCTGTAGA	268
Oy	331	AAATCGGAATGGGTTGATTAATTAATGATGATGCTTAAGGAGCTCTCGGTGAATTAAG	390
Db	269	AAATAGCGAATGCTTTTGATTAATCATCATGATGATGCCAAGCGTACGCTGATTAAGC	328
Oy	391	TCCTCCGCCATTTAGACCATGAAAATGTAATTTGGTTTAAGACACGTGATTCCTCACCT	450
Db	329	TTCTTAGGCAATTTAGATCATGAAAATGTCATTTGGTTTAAGAGATGTTATTCCTCACCT	388
Oy	451	TACGAAGGAGTTTCTGATGTTTACATTTGCTACTGAATCTCATGGATTTCTATCAC	510
Db	389	TGCGTTAGAGGTTTAAATGATGCTCATATACCAACCGAATCTGATGATCTTCAATC	448
Oy	511	AAATAAATTAATGCCAACCAAGTTTATCTAGAGATCACTGTAAGTCAATGATACGC	570
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Oy	571	TCCTCCGCGCTAAATATACATACATTTCCGGCAGATGTTCTCATGAGATCTCAACCGA	630
Db	509	TTCTTCGTGGACATGAGGTATATATACATTTCTGCAAACTTTTTCATGAGAAATTTGAAGCCA	568
Oy	631	GCAACCTTTGGTGAATGCACAAATTTGATCTTAAGATATGATGACTTTGCTCTGATAGC	690
Db	569	GCAATCTGTTGCTGAAATGCAAAATTTGGGACTTGAAGATTTTATTTTGGTCTTGGCGGC	628
Oy	691	CAAAATAGAGAACGAGATATAGCGAATATGTTGTTAAACGATGTTACAGGCAACCAG	750
Db	629	CAACATAGGAAAATGACTTCATACAGAAATATGATGATCAGAAATGATAGAGCTCTCG	688
Oy	751	AGCTTTGTTGAACCTCTTGATTAACAGCTGCTTAATATTTGGTCTGCGGTTGCA	810
Db	689	AATTTGTTGTAACCTCTCGATTTACACTCTGCTGCCATAGATTTTGGTCTGTTGGTTGTA	748
Oy	811	TCCTCATGGAACCTTATGAAATGAAGAACTTTGTTGGTGAAGAAAGATCATGTACATCAA	870
Db	749	TCCTCATGAGACTTATGAAATGAAGAACTTATTTCTGCGAAAGACCATGTGATCAGCA	808
Oy	871	TACGCTGTTAACCGACTCTTGGACCCCAAGAACGTGATGTTGGCTTCCCTCCAAA	930
Db	809	TGCGCTTATTAAGACAGACTCTTGGGACATCCCACTGACGCTATGTCGGTTAGTGAAGA	868
Oy	931	ATGAAGATGCAAGAGATATACATCAGGCACTCCACAAATCCTGCCAGCAGATTAGCAG	990
Db	869	ATGAAGATGCAAGAGATATATCCGCAACTTCCTCAATATCTCGCCAACTTTAANTA	928
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Db	929	GGGTTTTCCTCCCATGTTCAATCCCTTGGCCATCGATCTCATCATTAATAATTTGACAATTG	988
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Db	989	ATCCCATCAGAGATACAGTGGTGAAGAACACATGCCATCATCACTTGAAGAAACATAC	1048
Oy	1111	ACGATGAGAGTGAAGACCGATCGCTGTTCCATTTCTCTTTGACTTTGAGCAACAAG	1170
Db	1049	ACGATGTAGCTGATGAACCCATCTGCATGAGAACATTTCTCATTTGATTTGACAAACAGC	1108
Oy	1171	GAATAGAGAAAGAGCAAAATTAAGGACATGATATATACAGAAACCTTTGTCACGAACTCG	1230
Db	1109	ATTGAGACGAAGAGCAAAATTAAGAGATGATCTACAGGAGGACATTTACACCTCAATCTG	1168
Oy	1231	AATATGCTTAAC 1243	
Db	1169	AGTACGCTTAAC 1181	

AF386961	1480 bp	mRNA	linear	PLN 14-JUN-2001
LOCUS				
DEFINITION	Arbidiopsis thaliana	mitogen-activated protein kinase 3 (F9K21.220)		
ACCESSION	AF386961			
VERSION	AF386961			
KEYWORDS	complete cds.			
ORGANISM	Arbidiopsis thaliana.			
SOURCE	Arbidiopsis thaliana.			
REFERENCE	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots; Rosidae: eurosids II: Brassicales: Brassicaceae: Arabidopsis. 1 (bases 1 to 1480)			
AUTHORS	Lam, B., Southwick, A., Nguyen, M., Miranda, M., Palm, C. J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M. K., Hayashizaki, Y., Ishida, J., Kamiya, J., Kawai, J., Kim, C., Lin, J., Liu, S. X., Narusaka, M., Pham, P. K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R. W.			
TITLE	Direct Submission			
JOURNAL	Submitted (30-MAY-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA			
COMMENT	e-mail for correspondence: arab@sequence.stanford.edu			
	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.			
	The Salik, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Lam, B., Karlin-Neumann, G., Nguyen, M., Southwick, A., Miranda, M., Palm, C. J., Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M. K., Kim, C., Lin, J., Liu, S. X., Pham, P. K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R. W.			
	Iam, B., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R. W. (SSP/Stanford) contributed equally to this work as pIs.			
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Query Match	39.7%: Score 684; DB 8; Length 1480;			
Best Local Similarity	75.5%: Pred. No. 2.4e-150;			
Matches 849: Conservative 0; Mismatches 275; Indels 0; Gaps 0;				

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D	b	319	TACGGAGACAGCAACAGCTAGTAGCGAATGAAGAAATAGCTTAAGCTTTGTAATACATAT	378
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Best Local Similarity 71.1%; Pred. No. 1.2e-122;
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RESULT 15
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LOCUS
DEFINITION
ACCESSION
AF247136
VERSION
AF247136.1 GI:8925322
KEYWORDS
SOURCE
Capsicum annuum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
REFERENCE
1 (bases 1 to 1458)
Back,K., Han,O., Shin,H.-J. and Kim,K.-U.
Molecular cloning and cultivar specific expression of MAP kinase
from Capsicum annuum
Unpublished
2 (bases 1 to 1458)
Back,K. and Shin,D.-H.
Direct Submission
Submitted (18-MAR-2000) Genetic Engineering, Chonnam National
University, 300 Yeungpung-Dong, Kwangju 500-757, South Korea
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HM"

BASE COUNT      393 a      284 c      321 g      460 t
ORIGIN

Query Match      32.6%; Score 561.6; DB 8; Length 1458;
Best Local Similarity 70.6%; Pred. No. 1.5e-121;
Matches 763; Conservative 0; Mismatches 314; Indels 3; Gaps 1;
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Search completed: May 19, 2003, 22:21:28
Job time : 4383 secs

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Db 96 TAACATTCACGCCACGTTGAGTCAAGGCGGCTTATTCAATATACATATTTGGTAA 155
OY 215 TTTCTTTGAGATCAGTACCAAGTATGCTCTCTATTAATGCTTATGGTCGTGCTTA 274
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Db 156 TGTATTTGAAGTATGTCAAAGCTATAGCCCTCAATATATGCCAATGTGTAAGAGCCTTA 215
OY 275 TGGAAATGTCGTCGCGTGTGATACGAGCTGAATGAGTGGTTCAGTTAAGAAAT 334
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OY 1115 TGCAGGTGAGAACCGATCTGCCCTGTCCATCTCTCTTGTGATTTGAGCAACAAGAAAT 1174
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GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2003, 20:49:16 ; Search time 406 Seconds
(without alignments)
9568.219 Million cell updates/sec

Title: US-09-623-034-1
Perfect score: 1725
Sequence: 1 tatatacacatctgtctca.....gagcaagaagctgtgtata 1725

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1725	100.0	1725	18	AAT60349
2	1320	76.5	1786	18	AAT60350
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9	471	27.3	1546	21	AAC43674

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11	468.6	27.2	1119	22	AAC84253	Signal transductio
12	445.2	25.8	1282	21	AAC33580	Arabidopsis thalia
13	445.2	25.8	1359	21	AAC47261	Arabidopsis thalia
14	438.6	25.4	1116	21	AAC48312	Arabidopsis thalia
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16	416.4	24.1	1122	21	AAC42749	Arabidopsis thalia
17	378	21.9	1065	21	AAC42861	Arabidopsis thalia
18	337.2	19.5	1113	21	AAC43076	Arabidopsis thalia
19	335.6	19.5	1615	21	AAC48068	Zea mays DNA fragm
20	331.6	19.2	1138	21	AAZ98356	A. thaliana gene 1
21	330.8	19.2	1113	22	AAC84256	Signal transductio
22	330.8	19.2	1654	21	AAC44676	Zea mays DNA fragm
23	329.8	19.1	1131	21	AAC51150	Arabidopsis thalia
24	306.4	17.8	1307	21	AAC42374	Arabidopsis thalia
25	301.2	17.5	1719	21	AAC48025	Zea mays DNA fragm
26	298	17.3	1110	22	AAC84253	Signal transductio
27	294.4	17.1	953	24	ABA91063	Physcomitrella pat
28	289.6	16.8	1086	21	AAC42874	Arabidopsis thalia
29	265.2	15.4	1957	20	AAH86361	CDNA encoding mito
30	262	15.2	1770	21	AAC49947	Arabidopsis thalia
31	254	14.7	1627	22	AAH22558	P. patens MPK-1 en
32	248.6	14.4	1524	21	AAC41619	Arabidopsis thalia
33	247	14.3	1731	21	AAC45785	Signal transductio
34	246.6	14.3	2257	22	AAC4274	Arabidopsis thalia
35	244.2	14.2	1785	21	AAC42701	Arabidopsis thalia
36	244.2	14.2	1950	21	AAC45953	Arabidopsis thalia
37	233.6	13.5	1879	21	AAC49789	Arabidopsis thalia
38	233	13.5	1467	13	AAO20261	ERK2. Rat ratus.
39	233	13.5	1815	19	AAV71031	Green fluorescent
40	233	13.5	1818	19	AAV71023	Signal transductio
41	232.8	13.5	1635	22	AAC84283	Human CSAID bindin
42	232	13.4	1100	20	AAZ11605	DNA encoding novel
43	232	13.4	3757	23	AAH8119	Human cDNA differe
44	232	13.4	3757	24	ABK8381	Human CSAID bindin
45	232	13.4	3774	20	AAZ11601	

ALIGNMENTS

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AC	AAT60349;
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DT	04-JUN-1997 (first entry)
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KW	Mitogen activated protein kinase; MAP; infectious specific protein;
KW	plant; jasmonic acid; ss.
OS	Synthetic.
PN	JP09065881-A.
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PD	11-MAR-1997.
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PF	29-AUG-1995; 95JP-0220935.
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PR	29-AUG-1995; 95JP-0220935.
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PA	(NORU) NORINSUISANSO NOGYO SEIBUTSU SHIGEN.
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DR	WPI; 1997-220416/20.
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PT	P-PSDB; AAM15512.
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PT	Wound-stress inducible MAP kinase - used to regulate the synthesis
XX	of jasmonic acid
PS	Claim 5; Page 11-13; 21pp; Japanese.

XX Key Location/Qualifiers
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 FT /product= "salicylic acid induced MAP kinase"
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 XX MO9818939-A1.
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 XX 07-MAY-1998.
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 XX 24-OCT-1997; 97MO-US19219.
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 XX 21-APR-1997; 97US-0837593.
 XX 25-OCT-1996; 96US-0029805.
 XX
 XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
 XX
 XX Kiessig DF, Zhang S;
 XX
 XX WPI; 1998-272230/24.
 XX P-SDB; AAM61252.
 XX
 XX Salicylic acid induced MAP kinase - obtained from tobacco, used to
 PT produce plants having increased disease resistance, against e.g.
 PT microbial pathogens
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 XX Claim 11; Pages 21-22; 97pp; English.
 XX
 XX This cDNA encodes a salicylic acid induced protein (SIP) kinase. This SIP
 CC kinase is an unique member of the mitogen-activated protein (MAP) kinase
 CC family. The salicylic acid induced MAP kinase of the invention comprises
 CC kinase subdomains I to XI of serine/threonine kinases. The protein is
 CC activated by an agent that induces a disease defence response in plants
 CC by way of a signal transduction pathway that is at least partially
 CC dependent on salicylic acid. Host plant cells transformed with a vector
 CC containing a recombinant DNA molecule encoding the salicylic acid induced
 CC MAP kinase is used to produce the protein recombinantly. The products can
 CC be used to produce plants with increased disease resistance. The products
 CC may also be used as a research tool to identify other proteins involved
 CC in the hypersensitive response and systemic acquired response in plants.
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 XX Sequence 1544 BP; 449 A; 294 C; 335 G; 466 T; 0 other;
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 Best Local Similarity 70.1%; Pred. No. 1; Le-138;
 Matches 757; Conservative 0; Mismatches 320; Indels 3; Gaps 1;

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 Qy 575 CCGAGGCCCTAAATPACATACATTCGCGAATGTTCTTCATAGAGATCTCAACGAGCAA 634
 Db 641 CCGAGGTTAAATACATACATTCGCGAATGTTCTTCACAGGACTTGAAAGCTTGACAA 700
 Qy 635 CTTTGGTAAATGCAAAATGATCTTAAAGATATGATGATCTTGGTCTGAGGCCAA 694
 Db 701 TCTCCTGTGAATGCCAACTGTGATTTAAAGATATGATGATTTGGGCTGCTGTGAC 760
 Qy 695 CATAGAAAGAGATATGACGGAATGTTGTGAACCAATGTTACAGGACGACAGCT 754
 Db 761 TTCTGAATGCTATTATGACGAATATGTTGTGACAAATGTTATGCTCAGCTGAGCT 820
 Qy 755 TTGTTGAATCTTCAATATACATGCTGCTATAGATGTTGCTGCTGCTGCTGCT 814
 Db 821 GTTGTAAATTCGCTGACATATCTGACGAATGTTGACGATGTTGCTGCTGCTGCT 880
 Qy 815 CATGGAACCTTATGAAATGAAACCTTTGTTGGTGAAGAAATCATCATCATCAT 874
 Db 881 CATGGAATGATGACAGAAACCCCTATTTCTGTGATGATACAGTACACAGCTGCG 940
 Qy 875 CTTCCTACCGAGCTTTCTGACACCCCAAGAGATGATCTGCTCTCCAAATGA 934
 Db 941 TCTTATATGAGAGTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 997
 Qy 935 AGATGCAAGAGATATCATCAGCAACTCCCAACATCTCCGACGAGTTAGCAGAGT 994
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 Qy 995 TTTCCTCATGAGAACCATTTGCTATGATCTTGTGATGAAATGTTGATTCATCC 1054
 Db 1058 GTTCCATGATGACACCACTGCAATGATCTGTCGAAATGCTGATCTTGTGATCC 1117
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 Qy 1115 TGCAGGTGAGAACCATTTGCTATGATCTTGTGATGAAATGTTGATTCATCC 1174
 Db 1178 TATATGAGAGAGAGCCATTTGATGATGATGATGATGATGATGATGATGATGAT 1237
 Qy 1175 AGGAAAGAGCAATTTAGGACATGATATCATGAGAAAGCTTTGCTGATGATGAT 1234
 Db 1238 TACGAGAGAACAGATGAGAGGCTGATTTACAGGAGTCTGCTGATTTATCTGATA 1297
 RESULT 4
 AAC84262
 ID AAC84262 standard; cDNA; 1197 BP.
 AC AAC84262;
 AC 19-MAR-2001 (first entry)
 DT
 XX Signal transduction protein encoding cDNA.
 DE
 XX Zea mays; maize; signal transduction protein; phytohormone; ethylene;
 KM auxin; cytokinin; gibberellin; immunogen; ss.
 XX
 XX Zea mays.
 OS
 XX
 XX Key Location/Qualifiers
 FH CDS 1..1197
 FT /*tag= a
 FT /product= "signal transduction protein"
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 XX WO200070059-A2.
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 XX 23-NOV-2000.
 XX
 XX 28-APR-2000; 2000MO-US11687.
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PR	23-APR-1999;	99US-0130510.
PR	23-APR-1999;	99US-0130892.
PR	28-APR-1999;	99US-0131449.
PR	30-APR-1999;	99US-0132040.
PR	30-APR-1999;	99US-0132407.
PR	04-MAY-1999;	99US-0132485.
PR	05-MAY-1999;	99US-0132485.
PR	06-MAY-1999;	99US-0132486.
PR	06-MAY-1999;	99US-0132487.
PR	07-MAY-1999;	99US-0132866.
PR	11-MAY-1999;	99US-0134256.
PR	14-MAY-1999;	99US-0134218.
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PR	14-MAY-1999;	99US-0134370.
PR	18-MAY-1999;	99US-0134766.
PR	19-MAY-1999;	99US-0134941.
PR	20-MAY-1999;	99US-0135124.
PR	21-MAY-1999;	99US-0135355.
PR	24-MAY-1999;	99US-0135629.
PR	25-MAY-1999;	99US-0136021.
PR	27-MAY-1999;	99US-0136392.
PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
PR	03-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137502.
PR	07-JUN-1999;	99US-0137724.
PR	08-JUN-1999;	99US-0138094.
PR	10-JUN-1999;	99US-0138540.
PR	10-JUN-1999;	99US-0138847.
PR	14-JUN-1999;	99US-0139119.
PR	16-JUN-1999;	99US-0139452.
PR	16-JUN-1999;	99US-0139453.
PR	17-JUN-1999;	99US-0139492.
PR	18-JUN-1999;	99US-0139454.
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PR	18-JUN-1999;	99US-0139458.
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PR	18-JUN-1999;	99US-0139461.
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PR	18-JUN-1999;	99US-0139750.
PR	18-JUN-1999;	99US-0139763.
PR	21-JUN-1999;	99US-0139817.
PR	22-JUN-1999;	99US-0139899.
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PR	23-JUN-1999;	99US-0140354.
PR	24-JUN-1999;	99US-0140695.
PR	28-JUN-1999;	99US-0140823.
PR	29-JUN-1999;	99US-0140991.
PR	30-JUN-1999;	99US-0141287.
PR	01-JUL-1999;	99US-0141842.
PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142399.
PR	08-JUL-1999;	99US-0142803.
PR	09-JUL-1999;	99US-0142920.
PR	12-JUL-1999;	99US-0142977.
PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
PR	16-JUL-1999;	99US-0144086.
PR	19-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	19-JUL-1999;	99US-0144332.
PR	19-JUL-1999;	99US-0144333.
PR	19-JUL-1999;	99US-0144334.
PR	19-JUL-1999;	99US-0144335.
PR	20-JUL-1999;	99US-0144352.
PR	23-APR-1999;	99US-0144632
PR	20-JUL-1999;	99US-0144684
PR	21-JUL-1999;	99US-0144614
PR	21-JUL-1999;	99US-0145086
PR	21-JUL-1999;	99US-0145088
PR	22-JUL-1999;	99US-0145085
PR	22-JUL-1999;	99US-0145087
PR	22-JUL-1999;	99US-0145088
PR	22-JUL-1999;	99US-0145089
PR	22-JUL-1999;	99US-0145192
PR	23-JUL-1999;	99US-0145145
PR	23-JUL-1999;	99US-0145218
PR	23-JUL-1999;	99US-0145524
PR	26-JUL-1999;	99US-0145576
PR	27-JUL-1999;	99US-0145913
PR	27-JUL-1999;	99US-0145918
PR	27-JUL-1999;	99US-0145919
PR	28-JUL-1999;	99US-0145951
PR	02-AUG-1999;	99US-0146386
PR	02-AUG-1999;	99US-0146388
PR	02-AUG-1999;	99US-0146389
PR	03-AUG-1999;	99US-0147038
PR	04-AUG-1999;	99US-0147204
PR	04-AUG-1999;	99US-0147302
PR	05-AUG-1999;	99US-0147192
PR	05-AUG-1999;	99US-0147260
PR	06-AUG-1999;	99US-0147303
PR	06-AUG-1999;	99US-0147416
PR	09-AUG-1999;	99US-0147493
PR		

CC and gibberellin, to effect developmental changes in plants and provide
 CC control of plant response to environmental stresses. They may also be
 CC used as probes or amplification primers in the detection, quantitation or
 CC isolation of gene transcripts, for detecting mutations in the gene, for
 CC monitoring upregulation of expression or changes in enzyme activity in
 CC screening assays of compounds, for detection of any number of allelic
 CC variants, or for site-directed mutagenesis in eukaryotic cells. They may
 CC further be used for recombinant expression of their encoded polypeptides,
 CC as immunogens in the preparation or screening of antibodies, and in sense
 CC or antisense suppression of genes in a host cell, tissue or plant. The
 CC proteins may be used in assays for enzyme agonists or antagonists, as
 CC immunogens or antigens to obtain antibodies specifically immunoreactive
 CC with the proteins. The present sequence represents a cDNA encoding a
 CC signal transduction protein of the invention.

xx Sequence 1125 BP; 241 A; 390 C; 317 G; 177 T; 0 other;

Query Match 28.6%; Score 494; DB 22; Length 1125;

Best Local Similarity 65.5%; Pred. No. 4.3e-123;

Matches 722; Conservative 0; Mismatches 380; Indels 0; Gaps 0;

Qy 132 GGTGGCGGTGGAGTCATTCCTCATTTTCTGGTTTAACTCAGCGCGGACAATAT 191
 Db 13 GCGGTGGAGCGAGCTCCGGTCCGAGTCCGGACAGCGTCCAGCGCGGCTTC 72
 Qy 192 GTACAGTTGATATTTTGTATTTCTTTGATCACTACCAAGATGCTCCTCATTT 251
 Db 73 CTGCGAGTACAACTTTTGGGCAACTGTTGAGATCAGCAGCAAGTACAGCCCCCATTC 132
 Qy 252 ATGCTATTGTTGCTGTGCTTATGGAATGTCCTCGGTGTTGAATACGAGCTGAAT 311
 Db 133 ATGCCATTCGGCGCGGCGCTACGGGATCGTCTCGTGATGAATCCGAGCAAG 192
 Qy 312 GAGATGGTTGAGTAAAGAAATCGCAATGCGTTGATATTTACATGATGATCTTAAGAG 371
 Db 193 GAGATGGTGGCCATAGAAGATGCGCAACGCCCTTGACAAACCATGAGACCCCAAGCCG 252
 Qy 372 ACTCTCCGTGAGATTAACTCCTCCGCACTTAGACATGAAGAAATGTAATGTTTAA 431
 Db 253 ACGCTCCGGGAGATCAAGCTGCTGAGGCACTCGACCAAGAACATCATCTCGCATCAGG 312
 Qy 432 GACGTGATTCCTCCACCTTACGAAGGAGTTTCTGATGTTACATTCCTACTGAATC 491
 Db 313 GACGTGATTCGGCGCGCTCCGCAAGCTTCAACGAGTGTACATCGGAGCGAGCTG 372
 Qy 492 ATGATGATGATCTTACCATAATTTAGATCCAAACCAAGTTTACAGAGATCACTGT 551
 Db 373 ATGGACAGGACCTGACCACTATCGGTCCCAACAGGAGCTCTCGAGGAGCACTCC 432
 Qy 552 CAGTACTCATGATACAGCTCCGTCGTCGCTTAAATACATATTCGCGAGATGTTCT 611
 Db 433 CAGTACTCATGATACCAATCTCCGCGGCTCAAGTACATCACTCCGCCAAGCTGATC 492
 Qy 612 CATAGAGATCTCAAAACGAGCAACCTTTGTAATGCAAAATTTGATCTTAAGATATGT 671
 Db 493 CACCGCAGCTCAAGCCCACTGCTGTGAGACGCCCAACTCGGAGCTCAAGATCTGC 552
 Qy 672 GACTTGGTCTTGTAGGCGCAAAACATAGAGACGAAATATAGCGAATATTTTAAAC 731
 Db 553 GACTTGGGCTGGCGCGCGCTCTCCGAGAGCGACATGATACGAGATCGTGTCAAG 612
 Qy 732 AGATGGTACAGGACACAGAGCTTTTGTGAATCTTCAAGTATCACTCTCTATAGAT 791
 Db 613 CGCTGTACCGCGCGCGCGAGCTGTCTCACTCAGCAGCACTACTCGCGGCGCATCAGC 672
 Qy 792 GTTGGTCTGCTGCTGATCTTCAATGAACTTATGAAACCTTTTGTGGTGA 851
 Db 673 GTCTGTCTGCTGCTGCTTCAATGAGCTCATCAACCGCAGCGCTCTTCCCGGA 732
 Qy 852 AAAGATCATGTACATCAATACGCTTGTAAACGAGCTTCTGGACCCCAACAGAGCT 911
 Db 733 CGGACCAATGTCACCAAGATGCGCTCATACCGAGGATGATGGAGCGCCACGAGCAT 792

Qy 912 GATCTTGCTTCCTCCAAATGATGCAAGAGATACATCAGGCACTCCCAACAAT 971
 Db 793 GAGCTCGGTTATTCGGAACGACGCGGGAAGTACATGCCCACTCCCGCAGTTC 852
 Qy 972 CCTCGCAGCACTATGACAGATTTTCCCTCATGTGAACCCATTGGCTATTTGTC 1031
 Db 853 CCGCGCGCGCGCTGCTGACCTGTTCCCGCGAGTACACCCGCTGCGCATCCATC 912
 Qy 1032 GATMAAATGTTACATTCATCTCTACTAGAAATTTACAGTGGAGAACATTAATCAT 1091
 Db 913 GAGCGGATGCTCACTTCAACCCGCTGACAGAGATCACAGTGAAGAGCGCTGAGC 972
 Qy 1092 CCTCACTTGCAGCAAGCTCCACGATGCGAGTGAACGATGCGCTTCCATTTCC 1151
 Db 973 CCGTACTTGGAAACGGCTACACGACGCGCCGACAGACCATCTGACAGGACCGCTTCG 1032
 Qy 1152 TTTGACTTTGAGCAACAGGAATAGGAGAGCAAAATTAAAGACATGATATACGAA 1211
 Db 1033 TTGCACTTGCAGCAGAGGCTCTGACGGAAGCAAAATGACGAGCTGATTTCAACGAG 1092
 Qy 1212 GCTTGTCACTGAATCCTGAAT 1233
 Db 1093 GCCATGGAATCAACCCCAACT 1114

RESULT 8
 AAC44071
 ID AAC44071 standard; DNA; 1525 BP.
 XX AAC44071;
 AC 18-OCT-2000 (first entry)
 DT XX
 DE Zea mays DNA fragment SEQ ID NO: 41517.
 XX
 XX Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway; metabolic;
 KW pathway; promoter; termination sequence; corn; ss.
 OS Zea mays subsp. mays.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 XX
 XX 25-FEB-2000; 2000EP-0301439.
 PF
 XX 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130591.
 PR 28-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 30-APR-1999; 99US-0132407.
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 PR 05-MAY-1999; 99US-0132485.
 PR 06-MAY-1999; 99US-0132486.
 PR 07-MAY-1999; 99US-0132863.
 PR 11-MAY-1999; 99US-0134256.
 PR 14-MAY-1999; 99US-0134218.
 PR 14-MAY-1999; 99US-0134219.
 PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
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PR 18-JUN-1999; 99US-0139454.
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PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139753.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
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PR 24-JUN-1999; 99US-0140635.
PR 28-JUN-1999; 99US-0140823.
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PR 01-JUL-1999; 99US-0141842.
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PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142350.
PR 08-JUL-1999; 99US-0142803.
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PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
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PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.

PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147392.
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PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
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PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
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PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
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PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161405.

PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 28.48; Score 489.2; DB 21; Length 1525;
Best Local Similarity 65.28; Pred. No. 9.8e-122;
Matches 719; Conservative 0; Mismatches 383; Indels 0; Gaps 0;

QY 132 GGTGCGGTGGAGGTCATTCCTGATTTCTTCCTTGCTTAACTACAGCGGGACAAAT 191
DB 115 GGCCTGGACGGAGCTCCGCTCGCGGATCCGGACAGCGTGGACGCGCGCGGCTTC 174
QY 192 GTACAGTTGATATTTTGGTAAATTTCTTGAGATCACTACCAAGTATGCTCTATT 251
DB 175 CTGAGATCAACATATTTGGCACTGTTGAGATCAGACACAGATACAGCCCCCATC 234
QY 252 ATGCTTATGTCGTGCTTATGGAATTTCTGCTCGGTGGAATACGAGCTGAAT 311
DB 235 ATGCCCATCGCGCGGCTTACGGGATCGTCTGCTGTGATGAACCTCGAGACGAG 294
QY 312 GAGATGGTTGAGTTAAGAAATGCGGAATGCTTGTATTTACATGATGCTAAGAG 371
DB 295 GAGATGGTGGCCATCAAAAGATGCGCCAGCCCTTGACAAACCATGAGCGCAAGCGC 354
QY 372 ACTCTCCGTGAGATTAAAGCTCTCCGCAATTAGACCATGAATAATGTAATGTTAGA 431
DB 355 ACAGCTCGGGAGATCAACAGCTGCTAAGGACCTCGACACGAGAAACATCATGGCATCAG 414
QY 432 GACGTGATCTCTCCACCCTTCGAAGGAGTTTCTGATGTTACATTTGCTACTGACTC 491
DB 415 GACGTGATCCCGCGCGCTCCGCGAGGCTTCAACGACGTGATCATCGGAGCGAGCTG 474
QY 492 ATGATATCTGATCTTCAACAAATATTAGATCAACCAAGTTTACGAGGATGACTAGT 551
DB 475 ATGACACAGGACCTGACACCATATCTCCGCTCCAGACGAGAGCTTCGAGAGAGCTCC 534
QY 552 CAGTACTTATGATATCAGCTCTCCGCTGCTTAAATATCATATCATCCGCAATTTCTT 611
DB 535 CAGTACTTCTGTACAGATCTCTCCGCGGCTCAAGTATCATCCACTCGGCCAAGCTGATC 594
QY 612 CATGAGATCTCAACACGACCACTTTTGTAAATGCAAAATGTAATGATATGATGT 671
DB 595 CACGCTGACCTCAAGCCGACCACTGCTGTGAACGCAACTGCACTCAAGATCTGC 654
QY 672 GACTTGTGCTTGTAGGCAAAACATAGAGAAGATATGAGGGAATATGTTGTATAC 731
DB 655 GACTTGGGCTGGCGCGCCCTCTCCGAGAGCGACATGATGAGATGAGTGTGTCAG 714
QY 732 AGATGATACAGGAGCAACGACCTTTTGTGAACCTTTCAGATTTACACTGCTATAGAT 791
DB 715 CGTGTGATACCGCGCGCCGAGCTGCTGCTCAATCCACGCACTCTCGCGGCATTCAC 774
QY 792 GTTGTGCTGTGCTGCTGCTTATGATGAACTTATGAATAAAAACTTTGTTGGTGA 851
DB 775 GTGTGTCCTGCGCTGCTGCTTATGAGCTCATCAACCCGCGCTCTTCCCGCA 834
QY 852 AAAGATCATGATGATCAAAATGCTTGTAAACCGCTTGTGGACCCCAAGAACT 911
DB 835 CGGACACCATGACACAGATGCGCTCTAATACAGAGTGATGCGGACCCCAAGCAT 894
QY 912 GATCTGGCTTCTCCAAATGAAGATCAAAAGATACATCAGGCACTCCACACAT 971
DB 895 GAGCTGGGTTGATCGGAGAGGAGCGGGAAGTACATGCGGCACTCCCGAGTTTC 954
QY 972 CCTGCGCAGCAGTTAGCAGAGTTTCCCTCATGTGAACCCATGTCATTTGATCTTTC 1031
DB 955 CCGGCGCGGCTTGTGTCAGGCTGTTCGCGGATGACGCCGTCGCTGAGACTCATC 1014

QY 1032 GATAAATGTGATCATGATCTAGTACAGAAATTACAGTGTGAGAAACATTAGATCAT 1091
DB 1015 GAGCGGATGCTCACCTTTAAACCCGCTCGAGAGATCAAGTGAAGAGCGCTGAGACAC 1074
QY 1092 CCGTACCTTGGCAAAAGCTCCACGATGACAGTGAAGACGATGCTGCTTCCATTCTCC 1151
DB 1075 CCGTACCTTGGCAAAAGCTCCACGATGACAGTGAAGACGATGCTGCTTCCATTCTCC 1134
QY 1152 TTTGACTTTGAGCAACAAGAAATGAGAGAGACAAATTAAGACATGATATACAGAA 1211
DB 1135 TTGCACTTTCGAGCAGCAGGCTCTTGACGGAAGCAAAATGAACAGCTGATTTCAACGAG 1194
QY 1212 GCTTGTCACTGAATCTGAAAT 1233
DB 1195 GCCATGAACTCAACCCCACT 1216

RESULT 9

AAC43674
ID AAC43674 standard; DNA; 1546 BP.

XX AAC43674;

DT 18-OCT-2000 (first entry)

XX Zea mays DNA fragment SEQ ID NO: 40086.

KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.

XX Zea mays subsp. mays.

PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 29-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

XX PR 08-APR-1999; 99US-0128234.

XX PR 16-APR-1999; 99US-0128714.

XX PR 19-APR-1999; 99US-0129845.

XX PR 21-APR-1999; 99US-0130077.

XX PR 23-APR-1999; 99US-0130449.

XX PR 23-APR-1999; 99US-0130510.

XX PR 28-APR-1999; 99US-0130891.

XX PR 30-APR-1999; 99US-0131449.

XX PR 04-MAY-1999; 99US-0132048.

XX PR 05-MAY-1999; 99US-0132484.

XX PR 06-MAY-1999; 99US-0132485.

XX PR 07-MAY-1999; 99US-0132486.

XX PR 11-MAY-1999; 99US-0132487.

XX PR 14-MAY-1999; 99US-0132488.

XX PR 14-MAY-1999; 99US-0134218.

XX PR 14-MAY-1999; 99US-0134219.

XX PR 14-MAY-1999; 99US-0134221.

XX PR 18-MAY-1999; 99US-0134370.

XX PR 19-MAY-1999; 99US-0134768.

XX PR 20-MAY-1999; 99US-0134941.

XX PR 21-MAY-1999; 99US-0135124.

XX PR 21-MAY-1999; 99US-0135353.

XX PR 24-MAY-1999; 99US-0135629.

XX PR 25-MAY-1999; 99US-0136021.

XX PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 18-JUN-1999; 99US-0139454.
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PR 23-JUN-1999; 99US-0140353.
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PR 24-JUN-1999; 99US-0140695.
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PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142380.
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Best Local Similarity 64.8%; Pred. No. 8.1e-117;
Matches 699; Conservative 0; Mismatches 380; Indels 0; Gaps 0;

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QY 1074 GAGGAAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1133
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RESULT 10
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XX 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 787.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
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XX EP1033405-A2.
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XX 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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RESULT 11
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ID AAC84253 standard; cDNA; 1119 BP.
AC AAC84253;
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DT 19-MAR-2001 (first entry)

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XX Signal transduction protein encoding cDNA.
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XX Zea mays; maize; signal transduction protein; phytohormone; ethylene;
KW auxin; cytokinin; gibberellin; immunogen; ss.
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XX Zea mays.
XX
XX Key Location/Qualifiers
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XX FT /*tag= a
XX FT /product= "signal transduction protein"
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XX WO200070059-A2.
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XX 23-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US11687.
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XX 14-MAY-1999; 99US-0134292.
XX 08-JUL-1999; 99US-0142996.
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XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Helentjaris TG;
XX
XX WPI: 2001-031929/04.
XX DR P-PSDB: AAB48044.
XX
XX
XX New signal transduction nucleic acids and encoded proteins useful for
PT regulating phytohormone expression, including ethylene, auxins,
PT cytokinins and gibberellin, to provide control of plant response to
PT environmental stresses -
XX
XX Claim 1; Page 83-85; 126pp; English.
XX
XX The invention provides Zea mays signal transduction proteins and encoding
XX nucleotide sequences. The nucleic acids are useful for regulating
XX expression of phytohormones, including ethylene, auxins, cytokinins,
XX and gibberellin, to effect developmental changes in plants and provide
XX control of plant response to environmental stresses. They may also be
XX used as probes or amplification primers in the detection, quantitation or
XX isolation of gene transcripts, for detecting mutations in the gene, for
XX monitoring upregulation of expression or changes in enzyme activity in
XX screening assays of compounds, for detection of any number of allelic
XX variants, or for site-directed mutagenesis in eukaryotic cells. They may
XX further be used for recombinant expression of their encoded polypeptides,
XX as immunogens in the preparation or screening of antibodies, and in sense
XX or antisense suppression of genes in a host cell, tissue or plant. The
XX proteins may be used in assays for enzyme agonists or antagonists, as
XX immunogens or antigens to obtain antibodies specifically immunoreactive
XX with the proteins. The present sequence represents a cDNA encoding a
XX signal transduction protein of the invention.
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XX Sequence 1119 BP; 290 A; 282 C; 268 G; 279 T; 0 other;
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XX Query Match 27.2%; Score 468.6; DB 22; Length 1119;
XX Best Local Similarity 64.9%; Pred. No. 3.1e-116;
XX Matches 693; Conservative 0; Mismatches 0; Gaps 0;
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DB 109 AAGTACGCCCCACCATCCGCCCATGCGTGGCGGCTCTGCGATGCTGCGCGGCT 168
QY 294 TTGAATACGAGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 353
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QY 354 TACATGATGCTAAGAGAGACTCTCGTGAATTAAGCTCTCCGCAATTAAGACATGAA 413

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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 25.8%; Score 445.2; DB 21; Length 1282;
Best Local Similarity 63.8%; Pred. No. 7e-110;
Matches 675; Conservative 0; Mismatches 383; Indels 0; Gaps 0;

QY 174 ACTCAGCGGAGACATATGTACAGTTGATATTTTGGTAATTTCTTGACATCCTACC 233
DB 78 ACACAGGGTGGCCGTATGTTGACGACAGCTTTATGACAACTCTTGAAGTTTCAGA 137
QY 224 AAGTATGCTCCTCATATATGCTTATGTCGTGCTGTGATTTGCAATTTGCTCGGTG 293
DB 138 AAGTATGCTCCTCATATGCTTATGTCGTGCTGTGATTTGCAATTTGCTCGGTG 197
QY 294 TTGAATACGAGCTGATGAGATGCTGACGTTAAGAAATGCGAATGCGTTGATATT 353
DB 198 GTGAAGTACGAGCTGAGAGAAAGTGTATTAAGAAATGCGAATGCGTTGATTAAC 257
QY 354 TACATGATGCTAAGAGAGCTCTCGTGAGATTAAGCTCTCCGCGATTTGACCATGAA 413
DB 258 ATCATGATGCTAAGAGAGCTCTAGTAATAATTAATCTTCAGCATATGATCATAG 317
QY 414 AATGTAATGTTTAAAGAGCTGATTTCTCCACCTTACGAAGGAGTTTCTGATGTT 473
DB 318 AAGCTTAAACCATCAAGATATTTGATAGACCTCCGCAACGAGATTTCTCATGATGTC 377
QY 474 TACATGCTACTGAACCTCATGATGATCTTACCAAAATTAATTAATGATCCACCAAGT 533
DB 378 TACATGCTATGAGTTAATGAGACACTGATCTTCAGCAAAATCTCCGTTAAACCAATA 437
QY 534 TTATCAGAGATCACTGCTGACTTATCATGTATCATAGCTTCCTCCGCGCTTAAATATATA 593

Db 438 CTGACCGAGTATCATGCGCTTCTCTAGTATACAGGCTTAAAGGGCTCAAAATACGTG 497
QY 594 CATTCGGGAATGTTCTTCATAGATCTCAACCGAGACACCTTTGGTAAATGCAAT 653
Db 498 CACTCGGCCACATATTCATCGATCTTAGGCCAAGCAAGTCTACTTAACTCGGAA 557
QY 654 TGTATCTTAAGATATGACTTGTGCTTGTAGGCCAACAATAGAGAACAGATATG 713
Db 558 AACGAGCTAAAGATGGATTTGGGCTTCAGAACAACTCCGACACAGCTCATG 617
QY 714 ACGAATATGTTGTAACCAATGTTACAGGACACAGCTTTGTTGAATCTTCAGAT 773
Db 618 ACTAATAATGCTGATCCGCTGTACAGGGCTCTCGATGCTCTTAAGTCTCAGAG 677
QY 774 TACACGTGCTATAGATGTTGGTCTGCTGCTCCTCAATCATGAACTATGATGA 833
Db 678 TACACCGCAGTATGATATTTGCTGTGCTGCTACCTCGGCAATCATGAGGGA 737
QY 834 AACCTTGTGTTGGTGAAGAAATCATGATCAATACCTGTTAAACGAGCTTCTT 893
Db 738 CAACCGTTGTTCCAGGCAAGATTTATGTTATCAGCTTAGGCTTAAACAGAGCTTGA 797
QY 894 GGCACCCCAACAGAGCTGATCTTGCTCTCCAAATGAAGATGCAAGATACATC 953
Db 798 GGCCTCTCAGCAATTCAGGCTCGCTCTCTGCACTGACAAAGCAAGATACGTC 857
QY 954 AGGCACTCCCAACAATCTCCGACAGATTAGCAGAAAGTTTCCCTCATGTAAACCA 1013
Db 858 AGGCACTCCGCAATTCAGGCAAGATTTATGTTATCTGTAATTCGCAAAATGCCACT 917
QY 1014 TTGCTATGATCTGTTGCAATTAATGTTGACATTCATCTACTAGAAATTAAGTT 1073
Db 918 ACGGCTATCGATTTGCTGAGAGATGCTCTTGTCTTAACCGGCACTCTCACTC 977
QY 1074 GAGGAGCATATGATCACTTCTTACCTGCAAGCTCCAGTGAAGTGAAGCAACCGATC 1133
Db 978 GATGAGAGCCCTGGCCATGCTTACTTACCTACCCGACCATGATGAGCAAGAACGGTTC 1037
QY 1134 TGCCCTGTTCCATCTCTCTTGTGACTTGAAGCAAGAAATAGGAAAGCAATTAAG 1193
Db 1038 TGTTCGACTCTCTTACAGTTTGAATTTGCAACATCTCTTTCACAGAAAGAACATTAAG 1097
QY 1194 GACATGATATATCAGAAAGCTTTGTCTACTGATCTCTGA 1231
Db 1098 GAGCTTATCTACAAGAGTCTGCAAAATTCATCTCTGA 1135

RESULT 13
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ID AAC47261 standard; DNA; 1359 BP.
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AC AAC47261;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 53162.
XX
KM Hybridisation assay; genetic mapping; gene expression control;
XX
KM protein identification; signal transduction pathway;
XX
XX metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123348.

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PR 21-APR-1999; 99US-0130449.
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PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
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PR 26-OCT-1999: 99US-0161361.
PR 28-OCT-1999: 99US-0161920.
PR 28-OCT-1999: 99US-0161992.
PR 28-OCT-1999: 99US-0161993.
PR 29-OCT-1999: 99US-0162142.

Query Match 25.8%; Score 445.2; DB 21; Length 1359;
Best Local Similarity 63.8%; Pred. No. 7.1e-110;

Matches 675; Conservative 0; Mismatches 383; Indels 0; Gaps 0;

QY 174 ACTCAGCGGGAACAATATGATGACGTTGATATTTTGTAAATTCCTTGGATCACTACC 233
Db 157 ACACACGGTGGCCCGCTATGTTCACTACAAAGCTTATGACAACTCTTTGAGTTTCCA 216
QY 234 AAGTATCGTCCTCCTATATATGCTATGTCGTGCTTATGAAATGTCCTCGGTG 293
Db 217 AAGTATGTCCTCCTATGTCCTATGTCCTATGTCCTATGTCCTATGTCCTATGTCCTG 276
QY 294 TTGAATACGAGCTGATGATGATGTCGACGTTAAACAAATGCGAATGCGTTGATTT 353
Db 277 GTGAACCTCAGTCTGAGAAAGGCGCTATTAAAGATGCGTATGCTTTGATTAAC 336
QY 354 TACATGATGCTAAGAGAGCTCCGCTGAGATTAAAGCTCCGCACTTATAGCATGA 413
Db 337 ATCATGATGCTAAGAGAGCGCTACGTGAATTAACCTTCAAGCATATGATCATGAG 396
QY 414 AATGTAATGGTTTAAAGAGCGTATTCCTCCAGCCCTTACGAAGGAGTTTCTGATGTT 473
Db 397 AAGCTTATACCATCAAAATATTTGAAGACCTCCGCAACGAGATATCTTCATATGATG 456
QY 474 TACATGCTACTGAACTACTGATGATGATCTTACCAAAATTAATGATTCACACAGT 533
Db 457 TACATGCTATGATGATTAATGACACTGATCTTACCGAATCCTCGTTCTAACCAACA 516
QY 534 TTATCAGAGATCAGTGTAGTACTGATGATGATGATGATGATGATGATGATGATGAT 593
Db 517 CTGACCAAGTATCAATGCGGTTTCCATGATACCAAGCTTTAAGAGGCGCTCAAAATG 576
QY 594 CATTCGCGAATGTTCTTATAGAGATCTCAAAACGAGCAACCTTTTGGTAAATGCAAT 653
Db 577 CACTCGCGCAACATATTAATCATGCTGATCTTAAGCCCAAGCAACGCTTACTTAACTG 636
QY 654 TGTGATCTTAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 713
Db 637 AAGGACCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 696
QY 714 ACGAATATGTTGTAACGATGATGATGATGATGATGATGATGATGATGATGATGAT 773

Db 697 ACTGAATATGCTTACCCGTTGGACAGGCGCTCTGATGCTTCTTAATCGTCACAG 756
QY 774 TACACTGCTGATAGATGTTGGTCTGTCGTTGCATCTTACGAACTATGATGA 833
Db 757 TACACCGAGGTATGATTTGGTCTGTTGCTGCATACGCGGAATATGACGGGA 816
QY 834 AACCTTGTGGTGGAAAGATCATGTACATCAATACCTGTTAAACGAGCTTCTT 893
Db 817 CAACCGTGTTCAGCGAAAGATTATGTTATCATGCTTAAGCTTAACAGAGCTTGA 876
QY 894 GGCACCCCAAGAGAGTGTGCTTGGCTTCTCCAAAATGAAGATGCAAGATATATC 953
Db 877 GGCCTCTCAGCAATTCAGCGCTGCGCTTCTTGCAGTGAACAAGCAAGATATCCTC 936
QY 954 AGGCACTCCCAACAATCCCGCAGAGTTAGCAGAAAGTTTCCCATGTAACCCA 1013
Db 937 AGGCAACTCCCGCATCCCAACAACAGTTTGTCTGATTAATCCGAAATGCCCCACT 966
QY 1014 TTGCTATGATCTGTGATMAATGTTGACATTCCTACTAGAAATTAACAGTT 1073
Db 997 ACGCTATGATTTGCTTGAAGATGCTGCTTGTATCTTAACCGGCGATCTCATCTC 1056
QY 1074 GAGGAGCATTAATGATCATCTTACCTTGCAGAACTCCAGATGCAAGTGCAGAACCGATC 1133
Db 1057 GATGAAGCCCTTGGCCTGATCTTACCTATCACCGACCATGATGTGGCCAAAGAACCGGCTC 1116
QY 1134 TGCCCTGTGATCTCTCTTGTGATGAGCAACAAGAAATAGAGAGCAATTAAG 1193
Db 1117 TGTTCAGACTCTTTCAGCTTGTGATTTGCAACATCTTCTTGCACAGAAACACATTAAG 1176
QY 1194 GACATGATATATCAGAGAGCTTGTGATCTGATCTCTGA 1231
Db 1177 GAGCTTATCTCAAGAGACTCTGCAATTAATCATCTCTGA 1214

RESULT 14
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ID AAC48312 standard; DNA; 1116 BP.
XX
AC AAC48312;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57021.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123348.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.
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PR 04-MAY-1999; 99US-0132484.
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 Db 826 AGACAGCTTCCACAGTACCCCTGACAGAACTTCTGTAGATTCACCAAACTGTGGCT 885
 Qy 1014 TTGGCTATTGATCTGTGCGATAAATGTTCACATTCGATCTTACAGAAATTAACAT 1073
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 Db 946 GATGAGCGCTGTGCGACCCATATTTGGCGCGCTGCATGATATCAACGAAACCGGTA 1005
 Qy 1134 TGCCCTGTCCATCTCTCTGATTTGAGCAACAGAAATAGGAGAAACCAATTAAG 1193
 Db 1006 TGTGTGAGCGCTTCAATTTGATTTGAGCAACCTTACTTTGACAGAAAGAACATTAAG 1065
 Qy 1194 GACATGATATATCAGAAAGCTTGTCTCACTGAATCCTGAAATA 1234
 Db 1066 GAGCTTATATACCGTGAACAGTCAAGTTCATCTCAAGA 1106

RESULT 15
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 ID ABA91076 standard; cDNA; 1718 BP.
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 AC ABA91076;
 DT 22-FEB-2002 (first entry)
 XX
 DE Physcomitrella patens MPK-2 full-length cDNA, SEQ ID NO:21.
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 KW Protein kinase stress-related protein; PKSRP; moss; protein kinase-6;
 KW PK-6; protein kinase-7; PK-7; protein kinase-8; PK-8; protein kinase-9;
 KW PK-9; casein kinase homologue-1; CK-1; casein kinase homologue-2; CK-2;
 KW casein kinase homologue-3; CK-3; mitogen-activated protein kinase;
 KW MAP kinase-2; MPK-2; MAP kinase-3; MPK-3; MAP kinase-4; MPK-4;
 KW MAP kinase-5; MPK-5; calcium-dependent protein kinase-1; CPK-1;
 KW calcium-dependent protein kinase-2; CPK-2; overexpression;
 KW environmental stress; salinity; drought; temperature; tolerance;
 KW transgenic plant; EST; expressed sequence tag; ss.
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 OS Physcomitrella patens.
 XX
 PN MO20017356-A2.
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 PD 18-OCT-2001.
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 PF 06-APR-2001; 2001MO-US11435.
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 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Da Costa Silva EO, Bohnert HJ, Van Thielén N, Chen R;
 PI Sarria-Millan R;
 XX
 DR WPI: 2002-049153/06.
 DR P-PSDB: AAMS2837.
 XX
 PT New protein, useful for increasing tolerance to environmental stress,
 PT comprises a Protein Kinase Stress-Related Protein selected from
 PT Protein kinases, Casein kinase homologs, MAP kinases or Calcium
 PT dependent protein kinases
 XX
 PS Claim 14; Fig 2H; 154pp; English.
 XX
 CC Sequences AAMS2830-AAMS2842 represent novel protein kinase stress-related
 CC proteins (PKSRPs) from the moss Physcomitrella patens, and sequences
 CC ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA
 CC sequences were obtained from expressed sequence tags (ESTs; ABA91056-

CC ABA91068) derived from Physcomitrella patens cDNA libraries. The PKSRPs
 CC of the invention comprise protein kinase-6 (PK-6), protein kinase-7
 CC (PK-7), protein kinase-8 (PK-8), protein kinase-9 (PK-9), casein kinase
 CC homologue-1 (CK-1), casein kinase homologue-2 (CK-2), casein kinase
 CC homologue-3 (CK-3), mitogen-activated protein kinase (MAP) kinase-2 (MPK-2),
 CC MAP kinase-3 (MPK-3), MAP kinase-4 (MPK-4), MAP kinase-5 (MPK-5),
 CC calcium-dependent protein kinase-1 (CPK-1), and calcium-dependent protein
 CC kinase-2 (CPK-2). When overexpressed, the PKSRPs are able to confer
 CC tolerance to environmental stresses such as salinity, drought,
 CC temperature, metal, chemical, pathogenic and oxidative stress.
 CC Physcomitrella patens PKSRP nucleic acids may be used to generate
 CC transgenic plants and seeds with increased tolerance to salinity, drought
 CC and temperature. The transgenic plants generated can be monocots or
 CC dicots and are especially maize, wheat, rye, oat, triticale, rice,
 CC barley, cotton, rapeseed, cassava, sunflower, tagetes, leguminous plants
 CC (e.g., soybean, peanut, Vicia species, alfalfa), solanaceous plants
 CC (e.g., potato, tobacco, aborigine, pepper, tomato), coffee, cacao, tea,
 CC Salix species, oil palm, coconut, perennial grasses and forage crops. The
 CC PKSRP nucleotide and proteins may also be used in evolutionary and
 CC protein structural studies and as markers for specific regions of
 CC the genome.
 CC
 XX
 SQ Sequence 1718 BP; 389 A; 419 C; 425 G; 485 T; 0 other:

Query Match 24.3%; Score 420; DB 24; Length 1718;
 Best Local Similarity 62.6%; Pred. No. 5; Ie-103;
 Matches 654; Conservative 0; Mismatches 390; Indels 0; Gaps 0;
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 Qy 234 AAGTATGCTCTCTATATATGCTATTTGCTGCTGCTTATGAAATTTGCTGCTG 293
 Db 490 AGTACAAAGCCACACACTTCGTCGATTTGGCGGAGCTTATGAAATGCTGTCTACTC 549
 Qy 294 TTGAATACGAGCTGAATGAGATGATGATGATTAAGAAATGCGAAATGCTTGATATT 353
 Db 550 TTTATATACCTTTACGGGAGAGAGATGCGGCTCAAAAAGATTGGAAACGCTTCGACAA 609
 Qy 354 TACATGATAGTATAGAGAGACTCCGAGATTAAGTTCCTCCGCAATTAAGACATGAA 413
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 Qy 474 TACATTTGCTACTGACATCATGATGATGATTTACCAAAATTAATTAACACCAAGT 533
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 Qy 534 TTATCAGAGATCAGTCACTGATCTTATGATGATGATGATGATGATGATGATGATGAT 593
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 Db 910 TGCATTTGAAAACGAGATTTTGGCTTGGCAGCACTCTCTGTAAGCGATTTTCAGAT 969
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 Db 1030 TACACTGAGATATTAACATTTGCTGCTGGGAGCATCTTCACAGAGATTTTAACGA 1089
 Qy 834 AACCTTTGTTGGTGAAGAAAGATCATGATCATCAATATACCTTTGTTAACGAGACTTCT 893

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Db 1090 TCTCGTGTGTCCTCGGAGAGACTATGTGCATCAGCTCCGCCCTATTTACAGAACTCATC 1149
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Db 1150 GGAACCTCCTGAAGATAGGATCTTGGGTTTTTGAAGACGACAAATGCTAGCGGTATATC 1209
QY 954 AGGCACTCCCAACAACATCCTCGGCAGCAGTTAGCAGAAAGTTTCCCTCATGTGAACCA 1013
Db 1210 AAGCACTGCTCGACACAGTCCGCTATTCCCTTAACCCAGAAATTTCAGAGCATTTATCGT 1269
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Db 1330 GAAGCTGCTTGGCGCACCCCTTATTAGCTTCACTTCATGACATCAACGATGAGCCTGCC 1389
QY 1134 TGCCCTGTTCCATTCCTCTTGACTTGGAGCAACAAGSATAGAGAGAGCAAAATTAG 1193
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QY 1194 GACATGATATATCAGAACTTTG 1217
Db 1450 GATCTCATTTGGAGGAGGCTCTG 1473
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Job time : 414 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2003, 22:21:31 : Search time 241 Seconds
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Sequence: 1 tatatacaccatgtctca.....gagcaagagactgttgata 1725

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Searched: 810007 seqs, 644969091 residues

Total number of hits satisfying chosen parameters: 1620014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	531.8	30.8	1188	9 US-09-938-842A-644	Sequence 644, App
2	420	24.3	1718	10 US-09-828-313-21	Sequence 21, Appl
3	306.4	17.8	1107	9 US-09-938-842A-1471	Sequence 1471, Ap
C 4	294.4	17.1	953	10 US-09-828-313-8	Sequence 8, Appl
5	233	13.5	1815	9 US-10-072-036-58	Sequence 58, Appl
6	233	13.5	1818	9 US-10-072-036-40	Sequence 40, Appl
7	230.4	13.4	1821	9 US-10-072-036-64	Sequence 64, Appl
8	230.4	13.4	1824	9 US-10-072-036-46	Sequence 46, Appl
9	222.2	12.9	1611	9 US-10-171-311-126	Sequence 126, App
10	212.2	12.3	1308	10 US-09-801-368-149	Sequence 149, App
11	211	12.2	1869	9 US-10-098-841-114	Sequence 114, App
12	211	12.2	1875	9 US-10-072-036-56	Sequence 56, Appl
13	209.6	12.2	1551	9 US-09-938-842A-1067	Sequence 1067, Ap
14	209.4	12.1	1896	9 US-10-072-036-38	Sequence 38, Appl
15	202.8	11.8	1455	10 US-09-801-368-333	Sequence 333, App
16	173	10.0	4280	9 US-10-098-841-283	Sequence 283, App
17	170.2	9.9	1062	10 US-09-801-368-115	Sequence 115, App
18	168.2	9.8	1107	10 US-09-801-368-177	Sequence 177, App
19	168.2	9.8	1838	10 US-09-880-107-1547	Sequence 1547, Ap

20	163.2	9.5	1502	9 US-10-198-343-1	Sequence 1, Appl
21	163.2	9.5	1502	9 US-10-197-315-1	Sequence 1, Appl
22	161.2	9.3	444	10 US-09-770-444-820	Sequence 820, App
23	140.2	8.1	1780	9 US-09-861-097-17	Sequence 17, Appl
24	140.2	8.1	1780	9 US-09-861-098-17	Sequence 17, Appl
25	140.2	8.1	1873	9 US-09-954-531-155	Sequence 155, App
26	135.6	7.9	404	10 US-09-878-574-3791	Sequence 3791, Ap
27	130.4	7.6	1306	9 US-09-909-650A-22	Sequence 22, Appl
28	130.4	7.6	1422	9 US-09-908-650A-23	Sequence 23, Appl
29	130.4	7.6	1505	9 US-09-165-522-1	Sequence 1, Appl
30	130.4	7.6	1773	9 US-09-165-522-4	Sequence 4, Appl
31	130.4	7.6	2367	9 US-09-165-522-3	Sequence 3, Appl
32	130.4	7.6	2372	9 US-09-165-522-6	Sequence 6, Appl
33	130.4	7.6	2372	9 US-09-165-522-7	Sequence 7, Appl
34	129.8	7.5	372	10 US-09-878-574-1851	Sequence 1851, Ap
35	128.8	7.5	1418	9 US-09-861-097-11	Sequence 11, Appl
36	128.8	7.5	1418	9 US-09-861-098-11	Sequence 11, Appl
37	128.8	7.5	1893	9 US-10-072-036-62	Sequence 62, Appl
38	128.8	7.5	1902	9 US-10-072-036-44	Sequence 44, Appl
39	128.8	7.5	8750	10 US-09-776-167A-8	Sequence 8, Appl
C 40	126.6	7.3	462	10 US-09-770-444-395	Sequence 395, App
41	124.2	7.2	2522	9 US-09-165-522-11	Sequence 11, Appl
42	122.6	7.1	1975	9 US-09-165-522-9	Sequence 9, Appl
43	119.2	6.9	241	10 US-09-878-574-9048	Sequence 9048, Ap
44	116.2	6.7	400	10 US-09-960-352-5288	Sequence 5288, Ap
45	113.8	6.6	773	10 US-09-770-445-905	Sequence 905, App

ALIGNMENTS

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RESULT 1
US-09-938-842A-644
Sequence 644, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SAME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 644
LENGTH: 1188
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-644

Query Match          30.8%; Score 531.8; DB 9; Length 1188;
Best Local Similarity 69.0%; Pred. No. 1.2e+131;
Matches 744; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

157 ATTTCCTCGGTTTAACTACGCGCGCAATATGTAAGTTGATATTTTGGTAATT 216
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Db 104 AATTTCGCGGCACTTACCACTGGTGGTATTAATGATTAACATATTGGAAACA 163
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QY 217 TCTTTGAGATGACTACCAAGATCTGCTCATTAATAGCCTATGCTGCTGTATG 276
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QY	397	GCCATTATAGACCATGAAATGTATTTGGTTTAAAGAGACGTGATTTCCACCCCTTACGAA	456
Db	344	GTACATGATGATCAATGAAATAATTTGTTGCATTCAGAGATTTATATCCCGCACCATTAAGAA	403
QY	457	GGGAGTTTTTGTGATGTTTACATTTGCTACTGAACTCATGATATCTGATCTTCCACCAATATA	516
Db	404	ACGCTTTTCAACGATGTTTATACATCGGCTATGAGCTTAATGACACGTGATTCACATCAATACA	463
QY	517	TTAGATCCCAACAGGTTTATCAGAGAGATCACTGTACAGTACCTTCATGTAATGACGTCTCC	576
Db	464	TTCCGATCAATTCACACATTTATCCGAAGAACAATGTCGACGATATTTCTTTACAGATCTCC	523
QY	577	GTGCGCTAAATATACATACATTCGCGGAATGTTCTTCATAGAGATCTCAAAACGAGCAACC	636
Db	524	GTGGATTTGAAATATACATTCACCTCGCAAAATGTGCTTCACAGGATTTGAAACCAAGTAAATC	583
QY	637	TTTTGGTAAATGCAATTTGTGATCTTAAGATATGTGACTTTGGTCTTGGTATAGCCCAATA	696
Db	584	TCCTCCTGAAGCAACATCGCGACCTAAAAATGTGGATTTTGGGCTAGCTGACAGTCACTT	643
QY	697	TAGAGAACGAGATATATGAGAGCAATATGTTTGTAAACAGATGATACAGAGGACAGACACTT	756
Db	644	CTGAGAGGATTTTCAATGACTGAAATATGTTGTACAGAGATGATACCGTGCACAGACACTTC	703
QY	757	TGTTGAACTCTTCAGATTACACTGCTGCTATATAGATGTTTGGTGTGCGTGCATCTTCA	816
Db	704	TCTTAACTCTTCTATATATACCTGACAGCTATGATGATGTTTGGTGTGAGCTGTATATTCA	763
QY	817	TGGAATCTATGAAATGAAAAACCTTGTGTTGGTGGAAAAAGATATGATACATCAATACGCT	876
Db	764	TGGAGTTATGAGACCGTAAAGCACCCTTCCCTGAGAGATATATGCTCATCAGCTTCGCT	823
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QY	937	ATGCAAAAGATATACATCAGGCACTCCCAACAATCTCTCCGACAGCATTTAGCAGAAATTT	996
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QY	997	TCCCATGATGTAACCATATGCGCTATTTGATCTGTGATTAATATGTTGACATTCGATCCTA	1056
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RESULT 2			
US-09-828-313-21			
: Sequence 21, Application US/09828313			
: Patent No. US2002005962A1			
: GENERAL INFORMATION:			
: APPLICANT: COSTA e SILVA, OSWALDO DA			
: APPLICANT: BOHNER, HANS J.			
: APPLICANT: THIELEN, NOCHA VAN			
: APPLICANT: CHEN, RUDYING			
: APPLICANT: SARRIA-MILLAN, RODRIGO			
: TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF			

	FILE OF INVENTION: USE IN PLANTS
	FILE REFERENCE: 16313-0032
	CURRENT APPLICATION NUMBER: US/09/828,313
	CURRENT FILING DATE: 2001-04-06
	PRIOR APPLICATION NUMBER: 60/196,001
	PRIOR FILING DATE: 2000-04-07
	NUMBER OF SEQ ID NOS: 128
	SOFTWARE: PatentIn Ver. 2.1
	SEQ ID NO 21
	LENGTH: 1718
	TYPE: DNA
	ORGANISM: Physcomitrella patens
	US-09-828-313-21
	Query Match 24.3% Score 420; DB 10; Length 1718;
	Best Local Similarity 62.6%; Pred. No. 1e-101;
	Matches 654; Conservative 0; Mismatches 390; Indels 0; Gaps 0.
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OY	234 AAGTATTCCTCCCTCATTTATGCCATTGTGCTGCTGCTTATGSAATTTCTGCTCGG 293
Db	
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OY	294 TTGAATACGAGACTAATAGATGGTTGCAGTTAAGAAAATGCGAATGCGTTGTATTT 353
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	610 AGGATCGATGCGAACCGAACACTGCTGGTAATAAATCTCTCCGGCATATGAGATCTGA 669
OY	414 AATGTAATTTGTTTAGAGACGTGATTCCTCCACCCTTAGAAGGAGAGTTTTCTGATGTT 473
Db	
	670 AACGTCGTTGCCATTACAGACATCAATGCTGCCCCCACTAGGAGAAATTTCAACGCGTG 729
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OY	534 TTATAGAGAGATCACTGCACAGACTTCATGTAAGCTCTCCGTCGGCTTAATAATACATA 593
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RESULT 3

Sequence 1471, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kireps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1471
LENGTH: 1107
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1471

Query Match	17.8%;	Score 306.4;	DB 9;	Length 1107;
Best Local Similarity	58.1%;	Pred. No. 1.7e-71;		
Matches 579;	Conservative 0;	Mismatches 411;	Indels 6;	Gaps 2;

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Db	250	AGGCATGTGAGCGATGAGAATGTATCGCCTTAAAGATGTATGTTGCCGTAATAGA	309
OY	456	AGGCAAGTTTCTGATGTTTACATGGTACAGACATCATGATATCTGATCTTCCACCAATA	515
Db	310	TCCAGTTTCAAGATGTTTATTGTTATGAGCTAATGATACTATCTTCATCAAGATT	369
OY	516	ATTAGATCCAACCAAGGTTTATCAGAGATCACTGTCAGTACTTCATGTATCAGCTCTC	575
Db	370	ATTAAATCTCTCAGCTCTCTTTTGATGATCAGTCAGCAAGTACTCTTGTTGAGTGGCTT	429

QY	576	CGGGCCCTAAATATGCATACACTCCCGGGANTGTTCTTCATATAGAGATCTCAAAACCCAGCAAC	633
Db	430	AGAGGCTGAAGTATCTTCAATCTCGCAAACTACATCTTACCCGGGATTTAAACCCGGGCAAC	489
QY	636	CTTTGGTAATGCAGAAATTTGATCTTTAAGATATGACCTTTGGCTCTTGAGGCCAAAC	695
Db	430	CTCTTAGTATATGGAACCTCGATCTCAGAGATTGTGGATTGGGGTTGGCGAAGAACGAC	549
QY	696	ATAGAGAACG---AGAAATATGACGGAATATGTTTAAACCATGATGTAAGGGCACCGAG	752
Db	550	CAAGGTATATGACAGTTCAATGACGTGATATGTTGTTACCGTTGGTACAGAGCACTGAG	609
QY	753	CTTTGTTGAACCTTCAGATTAACCTGCGCATATGATGTTGGCTGTGATGGTGCATC	812
Db	610	CTTCTCTTTGTTGTGATTAACCTATGGAACCTCATTGATGATGATGATGGTGGTTGGCAT	669
QY	813	TTTCATGGAATTAAGATATAGAAAACTGTTTGGTGTGAAAAAGATCATGATCATCAATA	872
Db	670	TTCCGGGAGATTTCTGGTAGGAACCCGATTTTCCAGGAAACGAAATGCTTATACAGCTT	729
QY	873	CGCTTTGTTAACCGAGCTTCTTGGCACCCCAACAGAAAGCTGATCTTGGCTTCTCCAAAT	932
Db	730	AAGCTAATCATCAACCGTTGTTGGTATACCAGCAAGAAATGATATTCGGTTATAGACAAAC	789
QY	933	GAAGATCAAAAGATATCATCATCAGGCAACGCCAACAAATCTCGGCACAGTTAGACAGAA	992
Db	790	CCGAAAGCTGGAAGGTTTATAAAGTCTCTTCCGTACTCAAGAGGAACATCATCTCCAAAT	849
QY	993	GTTTTCCCTATGTGAACCCATGGCTATTGATCTTTCGATATAAATGTGACATTCGAT	1052
Db	850	CTTTATTCACCAAGCCAACTCCTTAGCTATAGATTGTACAGAGGATCTTGTGTTGGAT	909
QY	1053	CTTCTCTGAGGAATTTACGTTTGGGAAGATTAAGATCATCCTACTCTGCAAACTCTCAC	1112
Db	910	CCAAACCAAGAAATCTGTGTAACCGATGGCGCTTTACACCGGTATATGCGGGGTGTTT	969
QY	1113	GATCGAGGTGACGAAAGCATCTGCCCTCTTCATCTCTCTTTGACATTTGACAAACAAGA	1172
Db	970	GATCCTTGATTCATCGCGCTCGCAACATGTCGCCAATCTCTCTGACATGATGAAACATG	1029
QY	1173	ATAGAGAAAGGCAAAATTAAGGACATGATATATCAG	1208
Db	1030	GAGGAAACCAGTATTAAGAGATGATGTAAGTAAAG	1065

RESULT 4

Sequence 8
Patent No. US20020059662A1
GENERAL INFORMATION:
APPLICANT: COSTA E SILVA, OSMALDO DA
APPLICANT: BOHNETT, HANS J.
APPLICANT: THELEN, NOCHA VAN
APPLICANT: CHEN, RUYTING
APPLICANT: SARRIA-MILLAN, RODRIGO
TITLE OF INVENTION: PROTEIN KINASE STRESS
TITLE OF INVENTION: USE IN PLANTS
FILE REFERENCE: 16313-0032
CURRENT APPLICATION NUMBER: US/09/828,313
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/196,001
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentl Ver. 2.1
SEQ ID NO 8
LENGTH: 953
TYPE: DNA
ORGANISM: Physcomitrella patens
US-09-828-313-8

Query Match	17.1%;	Score 294.4;	DB 10;	Length 953;
Best Local Similarity	62.4%;	Pred. No. 2.6e-68;		
Matches 477;	Conservative 0;	Mismatches 286;	Indels 1;	Gaps 1;

Dh 919 GCCCACCCGTAAGCTGAGCAGTATTATGACCCAAAGTGAAGAGCCCATTCGTGAGCAGCA 978
Qy 1146 TTCTCCTTGACTTGAGCAACAAAGAAATAGAGAGAAATTAAGACATGATATAT 1205
Dh 979 TTCAAGTTTGACATGAGCTGAGCAGCTTACCTTAAGAGAGAAAGCTCAAGAACTCATTTT 1038
Qy 1206 CAGAAAGCTTTGTCTACGTAATCTGTAATA 1234
Dh 1039 GAAGAGACTGCTCGATTCAGCAGCAGGATA 1067

RESULT 6
US-10-072-036-40
: Sequence 40, Application US/10072036
: Publication No. US20030082564A1
: GENERAL INFORMATION:
: APPLICANT: Ole THASTRUP
: APPLICANT: Sara BJORN
: APPLICANT: Soren TULLIN
: APPLICANT: Kasper ALMHOLT
: APPLICANT: Kurt SCUDDER
: TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
: FILE REFERENCE: 3759-0120P
: CURRENT APPLICATION NUMBER: US/10/072,036
: PRIOR FILING DATE: 2002-09-13
: PRIOR APPLICATION NUMBER: 09/417,197
: NUMBER OF SEQ ID NOS: 143
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 40
: LENGTH: 1818
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: EGFP-Erk2 fusion
: NAME/KEY: CDS
: LOCATION: (1)..(1815)
US-10-072-036-40

Query Match 13.5%; Score 233; DB 9; Length 1818;
Best Local Similarity 55.2%; Pred. No. 9.1e-52;
Matches 546; Conservative 0; Mismatches 425; Indels 18; Gaps 4;

Qy 258 ATTGTCCTGCTGCTTATGGAATTTCTGCTGGTGTGTAATACGAGAGCTGATGATG 317
Dh 826 ATCGGAGAAGGCGCTACGCGATGTTGTTCTGCTTATGATTAATCTCAACAAAGTTGCA 885
Qy 318 GTTGAGATTAGAAAATGCGAATCGTTTGATTTATGATGATGCTAAGAGAGCTGTC 377
Dh 886 GTTGCTATCAAGAAATC---AGTCTTTTGAGCACCAGAGCTACTGTGACGAAACCTTG 942
Qy 378 CGTGAGATTAAAGCTCTCCGCAATTTAGACATGAAAATGTAATTGTTTAAAGACGTG 437
Dh 943 AGAGAGATAAAAATCTCTACTGCGCTTCAGACATGAGAACATCATCGCATCAATGCAATC 1002
Qy 438 ATTCTCCACCCCTTAGAAGGAGTTTCTGATGTTTACATTTGCTACTGCAATCTCATGAT 497
Dh 1003 ATCCGGGACCAACCATTTAGAGAGATGAAGATGATATATATAGTACAGAGACTCATGAG 1062
Qy 498 ACTGATCTTCAACAAATATTAATGATCAACCAAGGTTTATCAGAGATCATGTCAGTAC 557
Dh 1063 ACAGATCTTTACAAGCTCTGTGAAGACACAGCA---CTCAGCAATATGATCATTCGTCTAT 1119
Qy 558 TTTCATGATCAGCTCTCCGCGCTAAATACATACATTCGCGAATGTTCTTCATAGA 617
Dh 1120 TTTCATTATCAGATCTCTAGAGGATTAAAGTATATACATTCAGTAAAGTTCTGACCGT 1179
Qy 618 GATGCAAAAGCAGCAACTTTTGTGAATGCAATGTGAGCTTAAGATATGATGACTTT 677
Dh 1180 GACCTCAAGCTTCCAACTCTGCTGTAACACCACTGTGATCTCAAGATCTGTGACTTT 1239

Qy 678 GGTCTTGC---TAGCCAAACATAGAGAAGAGATA-----TGACGGAATATGTT 725
Dh 1240 GGCCTTGGCCCGTGTGTCAGATCCAGACCATGATCATACAGGGTTCTTGACAGATATGTA 1299
Qy 726 GTAACAGATGGTACAGGGCACCAGAGCTTTTGTGAACCTTCAGATTACATGCTGCT 785
Dh 1300 GCCACGCGTTGGTACAGAGCTCCAGAAATTAATGTAATTCAGGGTATATCAAGATCC 1359
Qy 786 ATGATGTTTGTGCTGTGCGTTGATCTTCATGAGAACTTATCAATAGAAAACCTTTGTT 845
Dh 1360 ATTGATATTGTTGCTGTGGGCTGCATCTGGCAGAGATGCTATCCACAGGCTTATCTTC 1419
Qy 846 GGTGAAAAGATCATGTATCATCAATATAGCTTTTAACCGAGCTTCTTGACACCCACACA 905
Dh 1420 CCAGGAAGCATTTACCTTGACCAAGCTGAATCATCTCGGATTTCTTGATCTCCATCA 1479
Qy 906 GAAGCTGATCTTGGCTTCTCCCAAAATGAAGATGCAAAAGATATCAGGCAACTCCCA 965
Dh 1480 CAGGAAGATCTGAATGTATTAATTAATTAAGGTAGAAACTATTTGCTTCTGCTCCG 1539
Qy 966 CAACATCTCGCCAGCAGTTACAGAGATTTTCCCTCATGTGAACCATTTGCTATTGAT 1025
Dh 1540 CACAAAATAAAGTCCGCGTGAACAAGTTTCCCAACGCTGACTCCAAAGCTCTGGAT 1599
Qy 1026 CTGTGATAAATGTTGACATTTGATCCTACTAGAGAATTAACAGTTGAGAGAGATTA 1085
Dh 1600 TTACTGATAAATGTTGACATTTTAACCTTCACAAAGAGATTTGAAGTTGAACAGCTCTG 1659
Qy 1086 GATCATCCCTACCTTGCAAAAGCTCCACAGATGAGGTGACGAACGATGCTGCTTGTCA 1145
Dh 1660 GCCACCCGTACTGAGAGAGATTAATGACCCAAAGTATGAGCCCATTCCTGAACAGCA 1719
Qy 1146 TTCTCCTTTGACTTTGAGCAACAAAGAAATAGAGAAAGCAATTAAGACATGATATAT 1205
Dh 1720 TTCAAGTTTGACATGAGCTGAGCATTTACCTTAAGAGAAAGCTCAAAAGACTCATTTT 1779
Qy 1206 CAGAAAGCTTTGTCACTGATCTGTAATA 1234
Dh 1780 GAAGAGACTGCTCGATTCAGCAGCAGGATA 1808

RESULT 7
US-10-072-036-64
: Sequence 64, Application US/10072036
: Publication No. US20030082564A1
: GENERAL INFORMATION:
: APPLICANT: Ole THASTRUP
: APPLICANT: Sara BJORN
: APPLICANT: Soren TULLIN
: APPLICANT: Kasper ALMHOLT
: APPLICANT: Kurt SCUDDER
: TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To A
: FILE REFERENCE: 3759-0120P
: CURRENT APPLICATION NUMBER: US/10/072,036
: PRIOR FILING DATE: 2002-09-13
: PRIOR APPLICATION NUMBER: 09/417,197
: NUMBER OF SEQ ID NOS: 143
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 64
: LENGTH: 1821
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: p38-EGFP fusion
: NAME/KEY: CDS
: LOCATION: (1)..(1818)
US-10-072-036-64
Query Match 13.4%; Score 230.4; DB 9; Length 1821;
Best Local Similarity 56.4%; Pred. No. 4.5e-51;

	Matches	495;	Conservative	0;	Mismatches	371;	Indels	12;	Gaps	3;
OY	255	CCTATTGGTCGTGCGTCTTATGAAGATTGTCTGCTCGGTGTTGAATAACGAGACTGAATGAG	314							
Dd	85	CCAGTGCGGCTCGGGGCCCTATGGCTCTGTGTGTGTGCTTTTGGACAACAAAACGGGGTTA	144							
OY	315	ATGTTGCAGTTAAAGAAAAATCGAATGCGTTTGGATTATTTACATGATGATGCTTAAGAGACT	374							
Dd	145	CGTGTGGCAGTGAAGAAGCTCTCCAGACCATTTCAGTGCATCATTCATCCGAAAAAGAAC	204							
OY	375	CTCCGTGAGATTAACTCTCCTCCGCCATTTAGACCATGAAAATGTAAATTGGTTTAAAGAGC	434							
Dd	205	TACACAGAACTCCGGTTACTTAAACATATGAACAACATGAAAATGATATTGCTGTGGAC	264							
OY	435	GTGATT----CTCCACCCCTTACGAAGGGAGTTTGTGATGTTTACATGTCCTCAACAC	491							
Dd	265	GTTTTTACCCCTCGAAGGTCCTGTGAGAGGAAATCAAATGATGTATCTGTGACCCATCTC	324							
OY	492	ATGATACTGATCTTCCACCMAATTAATTAGATCCAACCAAGTTTATTCAGAGGATCACTGT	551							
Dd	325	ATGGGGGCGAGATCTGMAACAACATGTGGAAAT--GTCAAGAACCTACAGATGACCATGTT	381							
OY	552	CAGTACTTCATATACAGTCTCCTCCGTGGCCCTAAAAATACATACATTCGCGCAATGTTCT	611							
Dd	382	CAGTTCCTTATCTACCAAAATTTCTCGAGGCTCAAAAGTATATACATTCAGCTGACATAAT	441							
OY	612	CATAGAGATCTCAAAACCGAGCAACCTTTTGGTAAATGCAAAATTTGATCTTAAGATATGT	671							
Dd	442	CACAGGAGACCTAAACCTAGTATCTAGCTGTGATGATGAAGACGTGTGAGTGAAGATTCTG	501							
OY	672	GACTTTGGTCTTGTCTAGAGCCAAACATAGAGAAGAGATATGACGGAATATGTTGAAC	731							
Dd	502	GATTTTGGACTGTGCTGGGACA-----CAGATGATGAATATGACAGGCTACCTGGCCACT	555							
OY	732	AATATGTACAGGGCACACAGAGCTTTTGTGTGAATCTCTTGATTTACACTGCTCTATTAAT	791							
Dd	556	AGTGTGTACAGGGCTCTCTGATGATCATGCTGAACCTGGATGATTTACAACACAGATTGAT	615							
OY	792	GTTTGGCTGTGCGTTGTCATCTTTCATGGAACCTTATGAATAGAAAACCTTTGTTGGTGA	851							
Dd	616	ATTTGTGTCAGTGGAGTGCATTAATGGCCGAGCTGTTGACTGGAAGAACATTTGTTCCGTG	675							
OY	852	AAAGATCATGTCAATCAAAATACGCTGTGTTAACCGAGCTCTTGGACCCCAACAGAAAGCT	911							
Dd	676	ACAGACCATATGATCTAGTTGAAGCTCATTTTAAGACTGTGTTGAACCCCAAGGGCTGAG	735							
OY	912	GATCTTGGCTCTCCAAAATGAAGATGCAAGAGATACATCAGGCAATCCCACAAACAT	971							
Dd	736	CTTTGAAGAAATCTCCTCAGAGTCTGGCAAGAACTATATTCAGTCTTGTGACTCAGANG	795							
OY	972	CCTGCGCAGCAATTAGCAGAAATTTTCCCTCATGTGAACCCATTGGCTATTTATCTTGTG	1031							
Dd	796	CCGAAGATGAACCTTTGCGAATGTATTATTGTGTGCCAAACCCCTGCTGTGCACTGGCG	855							
OY	1032	GATTAATATTGACATTCGATCCTACTAGAAATTAACAGTTAGAGAGACATTAAATCAT	1091							
Dd	856	GAGAAAGATCCTGTATNTGCACTCAGATTAAGABAATTTACAGCGGCCCAAGCCCTTGACAT	915							
OY	1092	CCCTACCTTGCAAAAGCTCCAGATGACGAGGTGACGAAC	1129							
Dd	916	GCCTACTTGTCTCAGTACCCAGATCCTGTGATGATGAAC	953							
RESULT 8										
US-10-072-036-46										
; Sequence 46, Application US/10072036										
; Publication No. US20030082564A1										
; GENERAL INFORMATION:										
; APPLICANT: Ole THASTRUP										
; APPLICANT: Sara BJORN										
; APPLICANT: Soren TULLIN										
; APPLICANT: Kasper ALMHOLT										
; APPLICANT: Kurt SCUDDER										

```

: TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To A
: TITLE OF INVENTION: On A Cellular Response
: FILE REFERENCE: 3759-0120P
: CURRENT APPLICATION NUMBER: US/10/072,036
: CURRENT FILING DATE: 2002-09-13
: PRIOR APPLICATION NUMBER: 09/417,197
: PRIOR FILING DATE: 1999-10-07
: NUMBER OF SEQ ID NOS: 143
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 46
: LENGTH: 1824
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: EGFP-p38 fusion
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1821)
: US-10-072-036-46

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Query Match	13.4%	Score 230.4	DB: 9	Length 1824
Best Local Similarity	56.4%	Pred. No. 4.5e-51		
Matches 495	Conservative	0	Mismatches 371	Indels 12
			Gaps	3
QY	255	CCTATTGGTCGCGAGCTTATAGAAATGTCTGCTCGGTGTGTAATACGAGCGAATGAG	314	
DB	826	CCAGTGGGGCTGTGGGGCCATATGCTCTGTGTGTGTGCTTTGGACACAAAAACGGGGTTA	885	
QY	315	ATGTTGCAGTTAAGAAAATCCGGAATGCGTTTGAATATTTACATGAGATCTAAGAGACT	374	
DB	886	CGTGTGGGAGTGAAAGAACCTCCAGACCATTTCATTCATTCATTCGCGAAAAAGAAC	945	
QY	375	CTCCCTGAGATTAACCTCCTCCGCACTTATAGCAATGAAATGTAAATGGTTTAAAGAAC	434	
DB	946	TACAGAGAACATCGGCTTACTTAACATATGAACAATGAAATGTATGTGTGTTGGAC	1005	
QY	435	GTGATT---CCTCCACCCCTTACGAAGGAGATTCTGTGATGTTTACATGTGCTACTGAATC	491	
DB	1006	GTTTTATACACCTCGAAGGTCCTGTGGAGAAATTCATATGATGTATCTGTGTGACCATC	1065	
QY	492	ATGATACTGATCTTCCACCAATTAATAGATCCAAACCAAGGTTTATCAGAGATCACTGT	551	
DB	1066	ATGGGGGAGAGACTCAACAAACATTTGTGAAT---GTCCAGAACCTTACAGATATACATGTT	1122	
QY	552	CAGTACTTCATGTATCAGCTCCGCTCGGTGACCTTAAATATCATATTCGCGCAATGTCCT	611	
DB	1123	CAGTTCCTTATCTACCAATTTCTCCGAGGTCTTAAAGTATATATCATTCAGCTACATAAT	1182	
QY	612	CATAGAGATCTCAACCGAGCAACCTTTTGTAAATGCCAATTTGTATCTTAAGATATGT	671	
DB	1183	CACAGGAGACCTTAAACCTAGTAACTAGCTGTGATGAAGAACTGTGAGCTGAAGATTCTG	1242	
QY	672	GACTTTGGTCTTGTACAGCCAAACATAGGAACGAAATATGACGGAATATTTGTAAAC	731	
DB	1243	GATTTTGGACGTGCTGCGGACA-----CAGATGATGAATATGACAGGCTACCTGGCCACT	1296	
QY	732	AGATGTCAGGGGACACAGAGCTTTTGTGTAGCTCTTACAGATTAACACTGCTCTATAGT	791	
DB	1297	AGGTGTACAGGGGCTCTGTGAGATCATGCTGAAGCTGTGATGATTAACACAGCACTTGAT	1356	
QY	792	GTTTGGTGTGTGCTGGTGCATCTTCAATGGAACCTTATGAATAGAAAACTTTGTTGGTGA	851	
DB	1357	ATTGTGTCAAGTGGATGATATATGCGCGAGCTGTGTGACGTAAGAAACATTTGTTCTGTGT	1416	
QY	852	AAAGATCATGTACATCAAAATACGCTTTGTTAACCGAGCTTCTTGGACACCCCAACAGACT	911	
DB	1417	ACAGACCATATTGATCACTGTAAGCTCATTTTAACTCTGTGGAAACCCACGAGGGCTGAG	1476	
QY	912	GATCTGGCTTCCTCCAAATATGAATGACGAAGATACATCAGGCACTCCACCAACAT	971	
DB	1477	CTTTTGAAGAAAATCTCTCTCAGAGTCTGCAAGAAACTATATTCAGTCTTTGACTCAGATG	1536	
QY	972	CTCTCCGACAGATTAGCAAGATTTTCCCTCATGTGAACCCATTGGCTAATGATCTGTCT	1031	


```

; SEQ ID NO 149
;
; LENGTH: 1308
;
; TYPE: DNA
;
; ORGANISM: Saccharomyces cerevisiae
;
US-09-801-368-149

```

Query Match	12.3%	Score 212.2	DB 10	Length 1308
Best Local Similarity	54.5%	Pred. No. 2.7e+6		
Matches 524	Conservative 0	Mismatches 413	Indels 24	Gaps 4

QY	202	ATATTTTGGTAATTTCTTTGGATGACCTACACAGTTCGTCCTCCATATATCCATTTG	261
Db	32	AGATATTTCGGTACAGGTTTGGAGATCTCAAAATGAT- --CAATGATTTAAACCCCGTTG	88
QY	262	GTCTGTGCTTATGGAATTGTCTCGTGGTGTGAATACGAGCTGAATGAGATGTTG	321
Db	89	GGATGGGGGCATTTGGTGGTTGGTTCACCGACGAGCACTTTGACATCTCACCGACTTG	148
QY	322	CAGTTAAGAAAATGCCAATTCGTTTATATTTCATGATGCTAAAGAGACTCTCCGTG	381
Db	149	CCATTAAAGAAAATCATGAAACCTTTTCCACTCGAGTCTGGCCAAAGGACATATCTG	208
QY	382	AGATTAGCTTCCTCCGCATTTAGCCATGAAAATGTATTTGGTTTAAAGACGTGATTG	441
Db	209	AACATAAACTCTAAACATCTTAAGACACGAGACTTGATTGCTCTTCAAGCAATATTTC	268
QY	442	CTCCACCCTTACGAAGGAGTTTCTGATGTTTACATTGCTACTGAACTCATGATGATG	501
Db	269	TTTCTCCATTGGAA- -----CATATATATTTTGTACAGGAAATTACAAAGAAAG	316
QY	502	ATCTTCACCAATTAATTAGATCCACCACAGTTTATCAGAGGATCACTGCACTACTTA	561
Db	317	ATTATACATAGACTCTTCCAAACA- -GACCTCTGAAAAGCAATTTGTTCACATATTTC	373
QY	562	TGTATACGCTCTCCGTGGCCCTAAATACATACATTCGCGAATGTTCTCTACAGAGATC	621
Db	374	TATACCAATTTCTAAAGGGTTTAAATATACGTTCACTCCGGGGCCGATTCATATAGATT	433
QY	622	TCAACCGAGCAACCTTTTGGTAATGCAAAATGTGATCTTAAAGATATGACTTTGGTC	681
Db	434	TGAACCGAGCAACATTCGTGATTAATGAAACTGTGATTTGAAGATTTTGGATTTGGTTC	493
QY	682	TTGTAGGCCAAACATAGAGACGAGAAATTGACGGAATTTGTTTAAACCAATGTTGATA	741
Db	494	TAG-----CAAGATTTCAGAGCCCTCAATGAGACAGGCTATGTTTCCACTATGATCTATA	547
QY	742	GGGACACAGAGCTTTTGTGAACTCTTCACATTTACACTGCTGCTATAGATGTTGGCTG	801
Db	548	GGGACACTGAAATATCTACTTAACGCGGCAAAATATGACGTGAGGTGCGACATTTGGTCCG	607
QY	802	TGCGTTGCATCTTCATGGAACCTTATGAAATGAAAACCTTTTGGTGGGAAAAGATCATG	861
Db	608	CTGCTGTGATTTTGGCGAATGATTAAGGTAAAGCTTTGTTCCCTGGGAAAGATCATG	667
QY	862	TACATCAATTAACGTTTGTAAACGAGCTTTTGGCACCCACAGAAAGCTGATCTTGGCT	921
Db	668	TTTCAACCAATTTTCGATCATCTGACTGTTGTGGGATCTCCGCCAAAGATGTGATTAATA	727
QY	922	TCTCCAAAATGAAGATGCAAGAGATACATACGCGCAACTCCCAACAACATCCCGCCACG	981
Db	728	CTATTGTTCGGAATAATCTCTAAATTTTTCCTTGTTTACCAACAGAGATCCAAATTC	787
QY	982	AGTTAGCAGAATTTTCCCTCATGTGTAACCCATTTGGCTATTTGATCTTGTCGATAAATGT	104
Db	788	CATTTCTGAAAGATTTTAAACAGTGCAGACTGATGCGGTAGACCTTTTGGAAAAATGCG	847
QY	1042	TGACATTGATCTCTAGAGAATTTACAGTTGAGAGAACATTAGATCATCCCTACCTTG	110
Db	848	TGCTTTTGGATCTTAAGAAAGAAATCACTCGCGCGGATGCTCTGGCTCATCTTATTGCG	907
QY	1102	CAAAAGCTCCAGATGCAAGGTGACGACAAACCGATCTGCCCCTGTTCATTTCTCTTGAATTTG	116
Db	908	CTCTTACCAAGATCCAAAGGATGAAACCACTAGCCGATGCGCAAGTTGATTTGGCACTTTA	967

QY	1162	A	1162
		1	
Db	968	A	968

RESULT 11
US-10-098-841-114
; Sequence 114, Application US/10098841

; GENERAL INFORMATION:

APPLICANT: Yang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Wang, Y. Wind

APPLICANT: Xu, Chongjun
APPLICANT: Zhou Ping

APPLICANT: Ma, Yunging
Wang, Jian-Pui

APPLICANT: Zhao, Qing A.
APPLICANT: Ren, Feiyan

APPLICANT: chen, Rui-hong
APPLICANT: Wang, Dunrui

;; APPLICANT: Wang, Zhiwei
;; APPLICANT: Wehrman, Tom

; APPLICANT: Zhang, Jie
; APPLICANT: Qian, Xiaohong

; APPLICANT: Drmanac, Radoj
; TITLE OF INVENTION: NO. US

```

; TITLE OF INVENTION: POLYMER
; FILE REFERENCE: 784CIP2
SUBJECT: POLYMERIZATION

```

; CURRENT APPLICATION NUMBER:
 ; CURRENT FILING DATE: 2002
 ; PRIOR APPLICATION NUMBER:

PRIOR APPLICATION NUMBER: ;
PRIOR FILING DATE: 2000-06-15 ;
PRIOR APPLICATION NUMBER: ;

PRIOR APPLICATION NUMBER: 2000-04

NUMBER OF SEO ID NOS: 331

```

; SOFTWARE: pt_FL_genes Vers
; SEO ID NO 114

```

```

; LENGTH: 1869
; TYPE: DNA
;

```

ORGANISM: Homo sapiens
FEATURE:

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; NAME/KEY: CDS
; LOCATION: (73)..(1212)
;

```

US-10-098-841-114

Query Match	12.
Best Local Similarity	53.
Matches	517.

malcomes 31/; conservative

214 ATCGCGAGCGCGGTACG

318 GTTGCACTTAAGAAATCG

Db 274 GTGGCCATCAAGAAAGATC-

QY 378 CGTGAGTTAGCTCCTCC

Db 331 CGGAGATCCAGATCCTGC

438 ATTCCTCACCCTTAGGA

Db 391 CTGGGGGCTCCACCTG

498 ACTGATCTTCACCAATAA

Db 451 ACTGACCTGTACAAGTTGC

OY 1206 CAGGA 1210
|1111|
Db 1099 CAGGA 1103

RESULT 13

US-09-938-842A-1067
; Sequence 1067, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krepes, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1067
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1067

Query Match 12.2%; Score 209.6; DB 9; Length 1551;
Best Local Similarity 53.5%; Pred. No. 1.5e-45;

Matches 493; Conservative 0; Mismatches 414; Indels 15; Gaps 2;

OY 257 TATTGTCGTGGCTTGAATGTCGCTGCTGTTGAATGAGAGTGAATGAGAT 316
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OY 557 CTTCATGATCAGCTCCCTCGTGGCTAAATACATACATCCGGAATGTTCTTCATAG 616
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Db 363 CTTCCTTGTACCAATCTCTCTGCTTAAATTTGATGACACCTGATGTTGCTCATAG 422
OY 617 AGATCTCAACCGAGCACTTTTGTAAATGCAAAATGATGATCTTAAGATATGACT 676
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OY 782 TGCTATAGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 841
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RESULT 14

US-10-072-036-38
; Sequence 38, Application US/10072036
; Publication No. US20030082564A1
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP
; APPLICANT: Sara BJORN
; APPLICANT: Soren TULLIN
; APPLICANT: Kasper ALMHOLT
; APPLICANT: Kurt SCUDDER
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To A
; TITLE OF INVENTION: On A Cellular Response
; FILE REFERENCE: 3759-0120P
; CURRENT APPLICATION NUMBER: US/10/072, 036
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/417, 197
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: Patent version 3.0
; SEQ ID NO 38
; LENGTH: 1896
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EGFP-Erk1 fusion construct
; NAME/KEY: CDS
; LOCATION: (1)..(1893)
US-10-072-036-38

Query Match 12.1%; Score 209.4; DB 9; Length 1896;
Best Local Similarity 53.5%; Pred. No. 1.9e-45;

Matches 516; Conservative 0; Mismatches 431; Indels 18; Gaps 3;

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|1111| |1111| |1111| |1111| |1111| |1111| |1111| |1111|
Db 898 ATGCGGAGGCGGCTACGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957
OY 318 GTTCAGTTAAGAAATCGCAATGCTTGAATTTACATGATGCTTAAGAGACTCTC 377
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Db 958 GTGCGCATCAAGAGATC---AGCCCTTGAACATCAGACCTCTGCGAGGAGCCTC 1014
OY 378 CGTAGATTAAGCTCTCCGCAATTTAGACCATTAATGTTGCTTAAAGAGACCTG 437
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Tue May 20 10:56:59 2003

us-09-623-034-1.rnpb

Page 12

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 Db 909 TCAAAAGAGATTTCCTGATGATGAGGCCCTGGAGCACTCTTACTGTCTATATGTGCATGA 968
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 Db 969 TCCAGCTGACGCAACCTGTGTGTAGTGAAGAAATTCGAAATTTAGTTTGA 1016

Search completed: May 20, 2003, 00:20:30
Job time : 259 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2003, 20:56:06 ; Search time 2257 Seconds
(without alignments)
12378.030 Million cell updates/sec

Title: US-09-623-034-1
Perfect score: 1725
Sequence: 1 tatataaccatgctctca.....gagcaaaagacttggtgata 1725

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthu: *
3: em_estin: *
4: em_estnu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hlc: *
9: gb_estl: *
10: gb_est2: *
11: gb_hlc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
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19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vit: *
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23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rtd: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	598.8	34.7	702	13	B1922618 EST542522
3	545.6	31.6	850	14	B0164817 EST610686
4	545.4	31.6	1715	11	AT108471 Zea mays
5	541.8	31.4	609	9	AT488693 EST247032
6	517	30.0	629	10	AM038184 EST279841

7	503.4	29.2	603	14	B0507523
8	503.4	29.2	675	12	BG597996
9	481.8	27.9	605	10	AM979631
10	471	27.3	1705	11	AT105588
11	465.6	27.0	712	10	AM776266
12	452.6	26.2	507	10	AM034815
13	450.6	26.1	699	10	AM775836
14	449	26.0	679	10	AM775829
15	447.2	25.9	672	10	AM684379
16	436.8	25.3	735	10	AM775798
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18	427.8	24.8	742	12	BG582359
19	413.4	24.0	685	10	AM773944
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21	406.2	23.3	713	10	BE662883
22	401.8	23.3	592	12	BE520309
23	392	22.7	687	12	BF644893
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35	373.8	21.7	863	10	BE412950
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ALIGNMENTS

RESULT 1
LOCUS BM409226 735 bp mRNA linear EST 22-JAN-2002
DEFINITION EST583553 tomato breaker fruit Lycopersicon esculentum cDNA clone
C1EG47N15 5' end, mRNA sequence.

ACCESSION BM409226
VERSION
KEYWORDS
SOURCE EST.

ORGANISM tomato.
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

REFERENCE 1 (bases 1 to 735)
Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai
,J., Bougri,O., Kirtness,E., Utterback,T., Van Aken,S., Roming
,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue, breaker stage (2002)
Unpublished (2002)
Contact: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.

FEATURES
Location/Qualifiers

Db	245	CGGAAATTAAGCTTCTTCCGCAATTTAAGCATTGAACCATGAAAGCAGTCATGTTTAAAGATGTG	304
OY	438	ATTCTCCACCCCTTAGAAGGAGGATTTTCATGTGTTACATTTGCTACTGAACCTCATGAT	497
Db	305	ATTCTCCGCGCCCTTAGCAAGGAGGATTTTCTGATGTTTACATTTGCTACTGAACCTCATGAT	364
OY	498	ACTGATCTTTCACCAATTAATAGATCCAAACCAAGTTTATACAGAGATCAGCTGTAGTAC	557
Db	365	ACTGATCTTTCACCAATTAATAGATCCAAACCAAGTTTATACAGAGATCAGCTGTAGTAC	424
OY	558	TTTCATGTATCAGCTCTCCGTCGCTCTAAATATACATACATTCGCGCAATGTCCTTCATAGA	617
Db	425	TTTCATGTATCAGCTCTCCGTCGCTCTAAAGTACATACATTCGCGCATGTTATTCATAGA	484
OY	618	GATCTCAAAACCGAGCAACCTTTTGGTAAATGCAAAATGTGATCTTAAAGATATGTGACTTT	677
Db	485	GATCTCAAAACCGAGTAAACCTCTTGCTAAATGCAAAATGTGATCTTAAATATGTGATTTT	544
OY	678	GCTCTGCTAGGCCCCAAACATAGAGAAAGCAAGATATGACGGAATATGTTGTAACCGAGATTT	737
Db	545	GCTCTGCTAGGCCCCAAACGTMAGAACGAGATATAGCAGATATGTGTAAACCGAGATGG	604
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Db	605	TACAGAGCACCAGAGACTTTTGTGTGAACCTTCAGATTACACGCGTCGCATAGATGTTTGG	664
OY	798	TCTGTGCGTGCATCTTCATGGAACTTATGAATAGAA	835
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LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BO164817		BO164817					1 (bases 1 to 850)	VandenBosch, K.,			
LOCUS	850 bp						Endre, G., Silverstein, K., Town, C.D., Van Aken, S.,				
DEFINITION	truncatula						Uterback, T., Cheung, F., and Fraser, C.M.				
ACCESSION	Medicago						The Medicago truncatula 'Kilcloone' set: ESTs selected and				
VERSION	truncatula						re-arranged from various libraries				
KEYWORDS	CDNA						Unpublished (2002)				
SOURCE	clone						Contact: VandenBosch, K.				
ORGANISM	PKVNC-1G8, mRNA						Department of Plant Biology				
							University of Minnesota				
							220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA				
							Tel: 612 624 2755				
							Fax: 612 625 1738				
							Email: kvandenbosch@umn.edu				
							TIGR sequence name: MTRNA807B Alias Clone name: KV0-1J2 More				
							information is available at: www.medicago.org				
							Seq primer: Skmod (CTA gaa CTA gtg gat CC).				
							Location/Qualifiers				
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/tissue_type="mixed tissues"
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/lab_host="XLDR"
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NotI; cDNA was prepared from polyA+ enriched RNA. The
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was directionally ligated into the Uniap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing CNA inserts were excised from the recombinant lambda-zap phage using Ex-assist helper phage and propagated in XLOR cells."

Query Match	31.6%	Score 545.6	DB 14	Length 850
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QY	271	CTTATGGAATTTCTCGCTCGG	TCTTGGAATACGAGCTGAATAGATGGTTGCAAGTTAAGA	330	271	CTTATGGAATTTCTCGCTCGG	TCTTGGAATACGAGCTGAATAGATGGTTGCAAGTTAAGA
Db	135	CTTACGGAAATCTTTGTTGCT	TGTTGGAATACGGAACAGATAGTTGGTTGCTGTGAAGA	194	135	CTTACGGAAATCTTTGTTGCT	TGTTGGAATACGGAACAGATAGTTGGTTGCTGTGAAGA
QY	331	AAATCGCGAATCGCTTGTGAT	TATTTACATGAGATGCTAAAGAGACCTCCGCTGATATTAAGC	390	331	AAATCGCGAATCGCTTGTGAT	TATTTACATGAGATGCTAAAGAGACCTCCGCTGATATTAAGC
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Db	255	TTCTTAAAGCATTAATCATG	AAATGTAATGTTTAAAGATGTTATTTCCACCAACCT	314	255	TTCTTAAAGCATTAATCATG	AAATGTAATGTTTAAAGATGTTATTTCCACCAACCT
QY	451	TACGAAAGGAGTTTCTGAT	GTGTTTACATGCTACTGAACTCATGGATACATGATCTTCACC	510	451	TACGAAAGGAGTTTCTGAT	GTGTTTACATGCTACTGAACTCATGGATACATGATCTTCACC
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Db	375	AAATCATTCGCTCTATCAAA	CAACCTGTGATGATGAACACGTCAGTACTTTTGTATCAGA	434	375	AAATCATTCGCTCTATCAAA	CAACCTGTGATGATGAACACGTCAGTACTTTTGTATCAGA
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Db	495	GCAACCTCGCTGTTAATGCA	AAATTTGATCTTAAGATATGTGACTTTGGTCTCTGCTAGGC	554	495	GCAACCTCGCTGTTAATGCA	AAATTTGATCTTAAGATATGTGACTTTGGTCTCTGCTAGGC
QY	691	CAACATATGAGACAGAAAT	TATGACGGATATGTTGTAAACAGATGTAACAGGCAACAG	750	691	CAACATATGAGACAGAAAT	TATGACGGATATGTTGTAAACAGATGTAACAGGCAACAG
Db	555	CAACATATGAGAAAGTACT	CATGACAGATAATGTTGTACGAGAAATGATATAGAGGCTCTCG	614	555	CAACATATGAGAAAGTACT	CATGACAGATAATGTTGTACGAGAAATGATATAGAGGCTCTCG
QY	751	AGCTTTTGTGAACCTCTCA	GATTTACAGTCTGCTATAGATTTTGGTCTGCGGTGCA	810	751	AGCTTTTGTGAACCTCTCA	GATTTACAGTCTGCTATAGATTTTGGTCTGCGGTGCA
Db	615	AATTTTGTGTAACCTCTCA	GATTTACAGTCTGCTATAGATTTTGGTCTGCGGTGCA	674	615	AATTTTGTGTAACCTCTCA	GATTTACAGTCTGCTATAGATTTTGGTCTGCGGTGCA
QY	811	TCCTCATGGAACCTTATGA	TAGAAAAAAGCTTTGTTGTGGAAGAAAGATCATGTACATCAA	870	811	TCCTCATGGAACCTTATGA	TAGAAAAAAGCTTTGTTGTGGAAGAAAGATCATGTACATCAA
Db	675	TTTTTATGAGCTTATGATA	TAAAAAGCCCTGTCTGTTCTGCGCAAAAGATCATGTGATCAAA	734	675	TTTTTATGAGCTTATGATA	TAAAAAGCCCTGTCTGTTCTGCGCAAAAGATCATGTGATCAAA
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QY	930	AATGAAATGCAAAAGATAT	CATCAGGCAACTCCCAACAACATCTCTCGCAGCAGTT	985	930	AATGAAATGCAAAAGATAT	CATCAGGCAACTCCCAACAACATCTCTCGCAGCAGTT
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ACCESSION	AY108471
VERSION	AY108471.1
KEYWORDS	HTC.
SOURCE	Zea mays.
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.
REFERENCE	Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Haneley,M., Morgante,M. and Tingey,S.V. Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes Unpublished (2002) 2 (bases 1 to 1715)
JOURNAL	Coe,E.C.
REFERENCE	Direct Submission Submitted (25-Apr-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
AUTHORS	Location/Qualifiers
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AUTHORS	/db_xref="taxon:457"
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Best Local Similarity	69.9%; Pred. No. 8,5e+105;
Matches 751:	Conservative 0; Mismatches 321; Indels 3; Gaps 1
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OY	292 TGTTGAATACGAGCGTGAATGAGATGGTTGCAGTTAGAAAATTCGGAGATGGCTTGATA 351
Db	327 CGCTCACTCCGAGACGGCAGGACGAGCGATCATCAAGAAGATTCGCCAACGCTTCGARA 386
OY	332 TTTCATCGAGATCTTAGAGAGACTCTCGTGAGATTAAAGCTCTCCGCCATTTAGACCATG 411
Db	387 ACAAGATGATGTCCAAAGCGCACGCTCCGGAGATCAAGTGTCTCCGCCACATGAGCAACG 446
OY	412 AAAAGTTAATGGTTTGAAGAGACGATTCCTCCCAACCCTTAGGAAGGGGCTTTTGANG 471
Db	447 AGAATATGTTGTCATTAAGAGATATCATACCTCTCCATTTGAGGGAGGCAATTCATGATG 506
OY	472 TTTACATTCGTAAGTAACTGATGATGATCTTCACCAAAATTAATTAGATCCAACCAAG 531
Db	507 TGTATATGCGCATGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 566
OY	532 GTTTATCGAGAGATACAGTCTGATCTTATCATATCAGTCTCTCGGTGGCTTAAATATCA 591
Db	567 CTTTGTCAGAGAGACGTCTGATTTTTCTTTATCAAAATTTCTGCTGCTGGAAGTATA 626
OY	592 TACATTCGCGGATCTTCTTCATAGAGATCTCAAAACCGCAACCTTTTGGTAATGCA 651
Db	627 TACATTCGCAAAATTTCTTCACGCTGATCAAGACCTTAGCAATCTTTCTTTGAATGCA 686
OY	652 ATTTGATCTTAAGATATGTGACTTTGGTCTTGATAGGCCAAACATAGAGAAGATA 711

Dd	687	ACTGTGACCTCAAGATTAISTGATTTTTGGCGTTTCGCCACCCTCAGAACTGATTTTA	746
OY	712	TGACGGAATATGTTTTTAACCCAGATGGTAGACGGCACACAGAGCTTTTGTTGAACCTCTTCG	771
Dd	747	TGACHTAATATGTGTGCACACAGATGSTATAGAGCACACAGAGCTTTTGTTGAACCTCCTCAG	806
OY	772	ATTACACGTGCTCTTACATGTTTGGTCTGTGGTTGCATCTTCATGACAACCTTATGATA	831
Dd	807	AATATACGTCTCCATTGATGTGTGTGTGTGGCTGTATATTTATGTAACCATGGACC	866
OY	832	GAAAACCTTTGTTGGTGGAAAAAGATGCATGCATCAATAATAGCGTTGTAAACCGAGCTTC	891
Dd	867	GAAAACCTTTGTTGTTCTGTGGAGAAGATCATGTCTCATCAGCTACGTCCTTTAAATGGAGCTCA	926
OY	892	TTGGCACCCCAACAGAAAGCTGATCTTGGCTTCCTCCAAAATGAAAGTGCMAAGAGATACA	951
Dd	927	TTGGCAGCGCAAAATGAGGGTGTATCTTGATTTTGT--AAATGAAATATGCAAGAGATATA	983
OY	952	TCAGCAACTCCCAACACATCCTCGCCAGCACTTAGCAGAGATTTTCCCTCAATGCAACC	1011
Dd	984	TCCGCCACTTCCTGTGTGATCACCCTTACAGCTCCTTACCTGAAAAATTTTCCACATGTACAC	1043
OY	1012	CATTGGCATATGATCTTGTCGATTAATAATGTGACATFTGCATCTCAGAACATTAACG	1071
Dd	1044	CTTTCGACATTTGACCTGGGAAAAAGATGCTACTTTTATCTTACACAGACAATTAACG	1103
OY	1072	TTGAGCAAGCATTAGATCATTCCTTACCTCTTGCACAAAGCTCCACAGATCAGAGTAGACGA	1131
Dd	1104	TTGAAGGGGCACTTGTCACACCCTTACTTGTCATCACTTCATGACATTAAGTATGAGCCAG	1163
OY	1132	TCTGCCCTGTTCATCTTCTTTCATCTTGACATTGTAGACCAACAGAAATAGGAGAAGCAAATTA	1191
Dd	1164	TCTGCTCATATGCCCTTTCAGCTTCGACTTCGACAGACATGSCATTATCTGAAGAACGATGA	1223
OY	1192	AGGACATGATATATACAGGAAGCTTTGTCCATATCTGTAATATGCTTTAAACATA	1246
Dd	1224	AGGATCTGATCTTACCAAGAGGCTCTTGCACTTAACCCAGATTACCAATGACCAAA	1278

RESULT 5	AI488693	609 bp	mRNA	linear	EST 18-MAY-2001
LOCUS	AI488693				
DEFINITION	EST247032 tomato ovary, TAMU Lycopersicon esculentum cDNA clone				
ACCESSION	AI488693				
VERSION	AI488693.1	GI:4384064			
KEYWORDS	EST.				
SOURCE	tomato.				
ORGANISM	Lycopersicon esculentum				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
	Assteridae; euasterids I; Solanales; Solanaceae; Solanum;				
	Lycopersicon.				
	1 (bases 1 to 609)				
	Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E,				
	, Liang,F., Upton,J., Konning,C.M., Craven,M.B., Fujii,C.Y., Bowman,				
	,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley				
	,S.D. and Giovannoni,J.				
	Generation of ESTs from tomato carpel tissue				
	Unpublished (1999)				
TITLE	Contact: CUGI				
JOURNAL	Clemson University Genomics Institute				
COMMENT	Clemson University				
	100 Jordan Hall, Clemson, SC 29634, USA				
	Email: http://www.genome.clemson.edu/orders/index.html.				
FEATURES	Location/Qualifiers				
source	1..609				
	/organism="Lycopersicon esculentum"				
	/cultivar="TA496"				
	/db_xref="taxon:4081"				
	/clone="cLED13D19"				
	/clone_1lb="tomato ovary, TAMU"				

Query Match	31.4%	Score 541.8;	DB 9;	Length 609;
Best Local Similarity	93.1%;	Pred. No. 5.5e-104;		
Matches 567; Conservative	0;	Mismatches 42;	Indels 0;	Gaps 0;

REFERENCE	1 (bases 1 to 629)
AUTHORS	D'Ascenzo, M., He, X., Lyman, J., Holt, I.E., Liang, F., Upton, J., Ronling, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksey, S.D. and Giovannoni, J.
TITLE	Generation of ESNs from tomato leaf tissue
JOURNAL	Unpublished (1999)
COMMENT	Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence.
FEATURES	Location/Qualifiers
SOURCE	1..629 /organism="Lycopersicon esculentum" /cultivar="Rio Grande Pfor" /db_xref="taxon:4081" /clone="cLEFID13" /clone_lib="tomato mixed elicitor, Bm1" /tissue_type="leaf" /dev_stage="4-6 week old plants" /lab_host="X11-Blue MR" /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; cLER - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenchone, ELX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."
BASE COUNT	183 a 117 c 130 g 199 t
ORIGIN	
Query Match	30.0%; Score 517; DB 10; Length 629;
Best Local Similarity	89.6%; Pred. No. 9, le-99;
Matches	569; Conservative 0; Mismatches 60; Indels 6; Gaps 1;
OY	112 TCATGGCTGATGCAAATAATAGGTGGTGGCGGTGACGTCATTCCCGATTTTCCTTGCGTTT 171
Db	1 TAATGGTAGTGCATTAATAGGTGGTGC-----TGCATCAATTCCTCATTTTCCATAAATTG 54
OY	172 TTAACACAGGGGGGCAAAATATGACTTACGCTTGAATTTTGGTAATTTCTTTGAGATCAGTA 231
Db	55 TCACATCATGCTGGACAATAATGTTCAAGTATGACATTTTGGTAATTTTGGAGATTACTA 114
OY	232 CCAAATATCGTCTCCCTTATATGCCATTATGGTCGCGTGTATGGAATTTGTCCTCGG 291
Db	115 ACAAGTATCAACCTCCTTCATCGATGCCATTATGGACGTGGGGCTTATGGAATTCGTGCTCG 174
OY	292 TGTTGAATACGAGACTGTAATGAGATGTTGCCAGTTAAGAAAATCGCGAATGCGTTTGATA 351
Db	175 TGTTTAAAGCCGAGCTGTAATGAGATGTTGGACGTTMAAAAATCCCAATGCTTTTGTGATA 234
OY	352 TTTCATCATGAGTCTAAGAGAGACTCCGCTGAGATTAACTCCTCCGCCATTAGACCATG 411
Db	235 ATTACATGAGATGCTAAGAGAGACGCTCCGTGAATTAAGCTTCTTCCATTAGACCATG 294
OY	412 AAAATGTAATTGGTTTAAAGAAGACGTATTCCTCCACCCCTTACGAAGGAGATTTTCTGATG 471
Db	295 AAACGCTATTGGTTTAAAGAGATGCAATTCCTCCGCCCTTACGAAGGAGAGTTTCTGATG 354
OY	472 TTTCATCATGACGTAACATCACTCATGATGATGATTCCTCACCAAATATTTAGATCCAACCA 531
Db	355 TTTCATCATGCTACTCACTCACTCATGATGATGATTCCTCACCAAATATTTAGATCCAACCA 414
OY	532 GTTTATCGAGAGATCAGTCACTCATGATGATGATCAGCTCCTCCGTGGCTAAATATACA 591
Db	415 GTTTATCGAGAGATCATTTGCACAGTACTCACTCATGATGATGATTCCTCCGTGGCTAAAGTACA 474
OY	592 TACATTCGGCGAATGCTTCTCATAGAGATCTCAACGAGACCAACTTTTGGTAAATGCAA 651
Db	475 TACATTCGGCGCATGTTATTCATAGAGATCTCAACCAACCAAGTAACCTTTGCTAAATATGCAA 534

OY	652	ATTGGAATCTTAAGATATAGTGCATTTGGTCCTTGACGCCAAACAATFAGAGAAGCAATA	711
Dd	535	ATTGTGATCTTAAGATATAGTGCATTTGGTCCTTGACGCCAAACAATFAGAGAAGCAATA	594
OY	712	TGACGAATATGTTGTGAACACAGATGGTACAGAGCA	746
Dd	595	TGACGAATATGTTGTGAACACAGATGGTACAGAGCA	629
RESULT 7			
LOCUS	BQ507523	603 bp	mRNA linear EST 22-JUL-2002
DEFINITION	EST14938 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STM0875'		
VERSION	BQ507523.2	GI:21923349	EST.
KEYWORDS	potato.		
SOURCE	Solanum tuberosum		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.		
REFERENCE	1 (bases 1 to 603)		
AUTHORS	Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C., Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and Karamchena,S.A.		
TITLE	Generation of a set of potato cDNA clones for microarray analyses		
JOURNAL	Unpublished (2002)		
COMMENT	On Jun 10, 2002 this sequence version replaced gi:2136392. Other ESTs: EST614939 Contact: Robin Buell The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: potatobtlgr.org This clone is available through the Research Genetics, contact the Research Genetics for further information 1-800-711-6195 or cdna@resgen.com Seq primer: T3.		
FEATURES	Location/Qualifiers		
Source	1..603		
	/organism="Solanum tuberosum"		
	/cultivar="Kennebec Or Bingle"		
	/db_xref="taxon:4113"		
	/clone="STM087"		
	/library="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"		
	/tissue_type="mixed tissues"		
	/lab_host="SOLR"		
	/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2: XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots."		
BASE COUNT	178 a	131 c	127 g 167 t
ORIGIN			
Query Match	29.2%	Score 503.4;	DB 14; Length 603;
Best Local Similarity	89.9%;	Pred. No. 6.7e-96;	
Matches 540;	Conservative 0;	Mismatch 61;	Indels 0; Gaps 0;
OY	670	GTAGATTTGGTCTTCTTGAGCCAAACATAGAGAACGAATTTGACGGAATATGTTGTA	729
Dd	2	GATGATTTGGTCTTCTTGAGCCAAACATAGAGAACGAATTTGACGGAATATGTTGTA	61
OY	730	CCAGATGGTACAGGGCACCAGACTTTTGGAACTCTTCAGATTACACTGCTGCTA	789
Dd	62	CCAGATGGTACAGGGCACCAGACTTTTGGTGAACCTTCAGATTACACTGCTGCTA	121
OY	790	ATGTTTGGTCTGCGGTTCGATCTTCATGAGAACTATGATATGAAAACCTTGTGTTG	849
Dd	122	ATGTTTGGTCTGCGGTTCGATCTTCATGAGAACTATGATATGAAAACCTTGTGTTG	181

FEATURES	Source
RESULT 8	
LOCUS	BG597996
DEFINITION	BG597996 675 bp mRNA linear EST 12-APR-2001
ACCESSION	EST496674 cSTS Solanum tuberosum cDNA clone cSTS19L21 5' sequence,
VERSION	BG597996
KEYWORDS	BG597996.1 GI:13616136
SOURCE	EST.
ORGANISM	potato.
	Solanum tuberosum
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	Asteridae; easterid I; Solanales; Solanaceae; Solanum.
REFERENCE	1 (bases 1 to 675)
AUTHORS	van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chelmingo,A.,
	Bougrit,O., Buehl,C.R., Ronning,C., Tanksley,S. and Baker,B.
	Generations of ESTs from sprouting potato eyes
	Unpublished (2000)
TITLE	Contact: Cathy Ronning
JOURNAL	The Institute for Genomic Research
COMMENT	For clone info: please contact Research Genetics, Libraries
	Division tel 1-800-711-6195, email cdra@resgen.com
	Seq primer: M13f-R.
	Location/Qualifiers
	1..675
	/organism="Solanum tuberosum"
	/cultivar="Kennebec"
	/db_xref="taxon:4113"
	/clone="cSTS19L21"
	/clone_1lb="cSTS"
	/rissue_type="sprouting eyes from tubers"
	/dev_stage="12-14 weeks post harvest"
	/lab_host="SOLR"
	/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2:
	XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
	taken from tubers. The tubers were incubated at 26C in the
	dark for 2-3 weeks prior to sprouting. The eyes were
	frozen in liquid nitrogen immediately upon removal from
	tubers."
BASE COUNT	192 a 149 c 137 g 197 t

ORIGIN

Query Match 29.2%; Score 503.4; DB 12; Length 675;
Best Local Similarity 89.9%; Pred. No. 6.6e-96;
Matches 540; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 670 GTGACTTGGTCTTGCTGCAAGCAACATATAGAGAACGAGAAATGTGACGGATATGTTGTA 729
|||||
Db 2 GTGATTTTGGTCTTGCTGCAAGGCCAAACCTAGAGACGAGAAATGTGACAGAAATGTAGTTA 61
QY 730 CCAGATGTACAGGGCACCAGAGCTTTTGTGAACCTCTTCAGATTACACTGCTGCTATAG 789
|||||
Db 62 CCAGATGTACAGGGCACCAGAGCTTTTGTGAACCTCTTCAGATTACACTGCTGCTATAG 121
QY 790 ATGTTTGGTCTTGCTGCTGCAATCTTCATGAGAACTTATGAAATGAAACCTTTGTTGG 849
|||||
Db 122 ATGTTTGGTCTTGCTGCTGCAATCTTCATGAGAACTTATGAAATGAAACCTTTGTTGG 181
QY 850 GAAAAGATCATGTATACATCAATATACGCTTGTATACCGAGCTTTGCGACCCCAAGAGAAG 909
|||||
Db 182 GAAAAGATCATGTATACATCAATATACGCTTGTATACCGAGCTTTGCGACCTCTACAGAAAT 241
QY 910 CTGATCTTGGCTCTCTCCAAAATGAGATGCAAGAGATACATCAGCACTCCCAACAC 969
|||||
Db 242 CTGATCTTGGCTCTCTCCAAAATGAGATGCAAGAGATATGTGACAGCACTCCCAACAC 301
QY 970 ATCCGCGCAGAGATTACAGAGATTTCCCTCATGTGAGAACCATTTGCTATGATCTTG 1029
|||||
Db 302 ATCCGCGCAGAGATTACAGAGATTTCCCTCATGTATTAATCCATTAAGCATTTGATCTTG 361
QY 1030 TCGATTAATGTGATCATTCGATCTCTACTAGAGAAATTAACATGAGAGAGATTAAGATC 1089
|||||
Db 362 TAGATTAATGTGATCATTCGATCTCTACTAGAGAAATTAACATGAGAGATTAAGATC 421
QY 1090 ATCCCTACCTTGGCAAGCTCCACAGATGCAAGAGATGCAAGCTGCTGTTCCATCT 1149
|||||
Db 422 ATCCCTACCTTGGCAAGCTCCACAGATGCAAGAGATGCAAGCTGCTGTTCCATCT 481
QY 1150 CCTTGAATTTGAGCAAGAGAAATAGAGAGAAATTAAGACATGATATATCAG 1209
|||||
Db 482 CTTTGCATTTTGGCAAGAGAGATGAGAGAGAGATTAAGACATGATATATCAG 541
QY 1210 AAGCTTGTCACTGATCATTCGATATGCTTAAACATTAAGAGAAATCAATTTCTTCC 1269
|||||
Db 542 AAGCTTGTCCGCTGATCTGATATGCTTAAAGCATTAAGAGAAATCAATTTCTTCC 601
QY 1270 T 1270
Db 602 T 602

RESULT 9
AM979631
LOCUS
DEFINITION
ESR341230 tomato root deficiency, Cornell University Lycopersicon
esculentum cDNA clone cLEM8M3 5', mRNA sequence.
ACCESSION
AM979631
VERSION
AM979631.1 GI:8171152
KEYWORDS
EST.
SOURCE
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.

REFERENCE
AUTHORS
1 (bases 1 to 605)
van der Hoeven,R.S., Garvin,D.F., Matera,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,R.S., Ronning,C.M., Craven,M.B., Bowman,C.L.,
Mierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Giovannoni,J.J.
and Tanksley,S.D.
Generation of ESTs from tomato nutrient-deficient roots
Unpublished (1999)
JOURNAL
COMMENT
Contact: CUGI

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.
Location/Qualifiers
1. 605
/organism="Lycopersicon esculentum"
/cultivar="TA96"
/db_xref="taxon:4081"
/clone="cLEM8M3"
/clone_lib="tomato root deficiency, Cornell University"
/tissue_type="roots"
/dev_stage="5-6 weeks old"
/note="vector: pBluescript SK-; Site_1: 5' EcorI; Site_2:
3' XhoI; supplier: Tanksley; tissue supplied by Dave
Garvin (USDA-ARS, Ithaca, NY 14850). Roots were harvested
from plants grown under the following
deficiencies/stresses: 10 mM Al, Zn, P, K, Fe, N), and
mRNA was isolated from individual treatments. Proportional
aliquots of mRNA of each treatment were mixed and used for
library construction."

BASE COUNT 170 a 112 c 125 g 198 t

ORIGIN

Query Match 27.9%; Score 481.8; DB 10; Length 605;
Best Local Similarity 90.1%; Pred. No. 2.4e-91;
Matches 516; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 138 GGTGAGAGTCAATTCCTGATTTTCTTCTGCTTTAACTCAGCGGAGCAATATGTACAG 197
|||||
Db 33 GGTGAGAGTCAATTCCTGATTTTCTTCTGCTTTAACTCAGCGGAGCAATATGTACAG 92
QY 198 TTTGATTTTGTGTAATTTCTTTAGATCACTACCAAGTATGCTCTATATGCTT 257
|||||
Db 93 TATGACATTTTGTGTAATTTCTTTAGATCACTACCAAGTATGCTCTATATGCTT 152
QY 258 ATTGCTGCTGCTTATGGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 317
|||||
Db 153 ATTGAGAGCGGCGCTTATGGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 212
QY 318 GTTGAGATTAAGAAATGCGAATCGTTGATTTATTCATGATGATGCTTAAGAGACTCTC 377
|||||
Db 213 GTTGAGATTAAGAAATGCGAATCGTTGATTTATTCATGATGATGCTTAAGAGACTCTC 272
QY 378 CGTAGATTAAGCTCTCCGCAATTTAGACATGAATAATGTAATTTGTTAAAGACGTG 437
|||||
Db 273 CGTAGATTAAGCTCTCTCCGCAATTTAGACATGAATAATGTAATTTGTTAAAGACGTG 332
QY 438 ATTGCTGCTGCTTATGGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 497
|||||
Db 333 ATTGCTGCTGCTTATGGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 392
QY 498 ACTGATCTTACCAATATATTGATTCACCAAGGTTTATCAGAGATCACTGCTAGTAC 557
|||||
Db 393 ACTGATCTTACCAATATATTGATTCACCAAGGTTTATCAGAGATCACTGCTAGTAC 452
QY 558 TTTGATGTATCAGCTCTCCGCTGCTTAAATATCATACATTTCCGCGAATTTCTTATAGA 617
|||||
Db 453 TTTGATGTATCAGCTCTCCGCTGCTTAAATATCATACATTTCCGCGAATTTCTTATAGA 512
QY 618 GATTCACCAAGAGAGACTTTTGTAAATGCAAAATTTGATGCTTAAGATATGAGCTTT 677
|||||
Db 513 GATTCACCAAGAGAGACTTTTGTAAATGCAAAATTTGATGCTTAAGATATGAGCTTT 572
QY 678 GGTCTTGTAGGCCCAACATAGAGAGAGAAAT 710
|||||
Db 573 GGTCTTGTAGGCCCAACATAGAGAGAGAAAT 605

RESULT 10
AY105588
LOCUS
AY105588 1705 bp mRNA linear HTC 25-MAY-2002

	DEFINITION	Zea mays PCO138354 mRNA sequence.		
	ACCESSION	AJ105568		
	VERSION	AJ105568.1 GI:21208666		
	KEYWORDS	HTC.		
	SOURCE	Zea mays.		
	ORGANISM	Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 1705) Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hainey,M., Morgante,M. and Tingey,S.V. Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes		
JOURNAL	TITLE	Unpublished (2002)		
REFERENCE	AUTHORS	2 (bases 1 to 1705) Coe,E.C.		
JOURNAL	TITLE	Direct Submission Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA		
FEATURES	Source	Location/Qualifiers 1..1705 /organism="Zea mays" /db_xref="MaizEDB:638122" /db_xref="taxon:4577" /clone="PCO138354" /clone_id="Maize Mapping Project/DuPont Consensus Library" /note="this sequence is part of a project of EST assemblies resulting from the application of public configs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACS in conjunction with the Maize Mapping Project"		
BASE COUNT	453 a	433 c	391 g	428 t
ORIGIN				
Query Match	27.3%	Score 471;	DB 11;	Length 1705;
Best Local Similarity	64.8%;	Pred. No.3.9e-89;		
Matches	699;	Conservative	0;	Mismatches 380; Indels 0; Gaps 0
OY	174	ACTCACGGCGGCAAAATAGCTTACAGTTTGATAATTTTTGGTAATTTCCTTTGAGATCACTACC	233	
Dd	316	ACGCACGGGGGGGGGTACTGCTGTACAACGGTACGGMAACCTTCCAGSGCTCTGCC	375	
OY	234	AAGTAGCGCTCCCATTTATTTGGCTTTGGTGGTGGGCTTATGAATTTCGTGCGTGGG	293	
Dd	376	AAGTAGCCCCCACCACCATCGGCCCATCGTCCGGCGGCGCTTACGGCATTTCTTGCGGGCT	435	
OY	294	TGTGAATACGGAGCTGAATAGATGGTTGCGATTAGAAGAAAATGCGAATCGTTTGATATT	353	
Dd	436	GTCACCTGCGACATCGAGGGAGGAGGTGGTGATCAAGAAAGTTGGCAATCGTTGCGAAC	495	
OY	354	TACATGAGATGCTTAAGAGACTCTCCGTGAGATTAAAGCTCTCTCCGCATTTAAGACATGAA	413	
Dd	496	CACATCGACGCCAACCGGACGCTCAGGGAAAAATCAAAGCTCTCGCCATGACCATGTAG	555	
OY	414	AATGTAATTGGTTTAAAGACGTGATTCCTCCACCCCTTACGAAGGAGGTATCTGATGTT	473	
Dd	556	AACATCTCTTGCTTTAAAGATATTAATTGGGCCCCCACACTAGAGAGACTTTAATGACGG	615	
OY	474	TACATGTCTACTGAACCTCATGATAGTATCTTCAACCAAAATATTAGATCCAACCAAGT	533	
Dd	616	TACATGTGTACTGAGATTATGATACAGATCTCCATCAATCATGATGTAOGCTCAATCAGCA	675	
OY	534	TTATCAGAGGACTACTGTCAGTACTTCATGTATCAAGCTCTCCGTGGCCTAAATACATA	593	
Dd	676	TTGACTGTATGATCAATTCGACGACTCTTCTGTATCAGTTGTTCACGAGGGCTAAATATG	735	
OY	594	CATTCGGGAATAGTCTCTCATAGAAATCTCAACCGAGAGCAACCTTTTGGTAATGAAT	653	
Dd	736	CACATGAGAAATATATTTGACCGCATCTGAAGCCGAGAGCAATTTTCTCTTAATGCAAT	795	

QY	654	TGTGATCTTAGATATGTGACTTTGGTCTTGCTAGGCCAAACATAGACAGAGATATG	713
Db	796	TGTGACCTCAACATGTGACACTTTGGGCTTGGCAAGACCACCTTCAGAACACATCTCATG	855
QY	714	ACGGAATATGTTGTACCAAGATGTACAGAGGACAGAGCTTTTGTCAACCTCTCAAT	773
Db	856	ACAGAGTATGTGTACTCTGTTGGTACCGGGACCCAGAGCTGCTTTGACCTGTTCAAG	915
QY	774	TACACTGTGCTATAGATGTTTGGATCTGTGGTTGCATCTTCATGAACTTATGAAATGA	833
Db	916	TATACTGCTGCATGTATGTCTGTGACAGTTGGATGCATACTAGTGAAATGCTTACTGCT	975
QY	834	AAACCTTTGTTGGTGGGAAAAAGATCATGTACATCAAAATACGCTTTTAAACGAGCTTCTT	893
Db	976	CAACCCCTGTTTCCGACAGGGGATTCATCCAGCAATTTAAATTTATCATCGAGCTCATTA	1035
QY	894	GGCACCCCAACGAAGAGCTGATCTTGCTTCCTCCAAATGAAAGATGCACAAAGATACATC	953
Db	1036	GGCTTCCAGATGATGACCAAGCTGGGATTTTCTTCCAAAGTGAATATGCAAAAAGATACATG	1095
QY	954	AGGCAACTCCCAACAACATCTCTGCCAGCAGTTAGCAGAAAGTTTTCCTCATGTGAAACCA	1013
Db	1096	AAACAATACCAACAGATTTCCAAAGACAGGACTCCGCTGCGGTTTCCGCAACATGCTCCT	1155
QY	1014	TTTGCTATTGATCTTGTGATAAATGTGGACATTCGATCCTACTAGAAAGATTACACTT	1073
Db	1156	GGCGGAGTCGATTTTGTGGAAAGAGTGGTGTGTTGATCCAAAGCAGGGTATTCACATT	1215
QY	1074	GAGGAAGATTATGATCATCTCCACTCTGCAAAAGTCCACGATGCAGGTGAGCAACCGATC	1133
Db	1216	CATGAGGCTCTGCATCATCATCTACTTGGCTTCACTTCAATGAGATCAATGATGAACTAC	1275
QY	1134	TGCCCTGTTCCATTTCTCCTTGACTTTGAGCAACAAGAAATAGAGAAAGCAATTAA	1193
Db	1276	TGCCCTGCACCTTGACGTTGATTTGAGCAACATCCTTTACAGAAAGCGATATAAA	1335
QY	1194	GACATGATATATACAGAAAGCTTTGTCACTGAATCTGTGAATATGCTTTAAACATTAAGAA	1252
Db	1336	GAACTCATCTGGAGGAATCTTTACATTTAAACCAAGAGCTCCCTACTATATATCAAAA	1394

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
AM776266	LOCUS	AM776266	DEFINITION	EST3353331 DSIL Medicago truncatula cDNA clone pDSIL-7E14, mRNA sequence.
AM776266	ACCESSION	AM776266	VERSION	AM776266
AM776266.1	KEYWORDS	GI:7766079	EST	
barrel medic.	SOURCE			
Medicago truncatula	ORGANISM			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.				
1 (bases 1 to 712)				
Pedorova,M., Pearson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.				
ESTs from leaves of Medicago truncatula after inoculation with Colletotrichum trifolii				
Unpublished (2000)				
Contact: Deborah A. Samac				
Department of Plant Pathology				
University of Minnesota				
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA				
Tel: 612 625 1243				
Fax: 651 649 5058				
Email: debbys@uccn1.crl.umn.edu				
Minnesota sequence name:M259599e				
TIGR sequence name:MTFAR3JTK				
More information is available at:				
http://chrystie.tamu.edu/medicago				

BASE COUNT	204 a	142 c	137 g	216 t	be of fungal origin."
ORIGIN					
Query Match					26.1%; Score 450.6; DB 10; Length 699;
Best Local Similarity					78.9%; Pred. No. 8.6e-85;
Matches 537; Conservative					0; Mismatches 144; Indels 0; Gaps 0;
QY	393	CTCGGCCATTAGACCATGAAAATGTATTTGGTTTAAAGACGATGATCTCCACCCCTTA	452		
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Db	61	CGTAGAGAGTTTAAATGATGTTTACATTAACACCGAAGCTCATGATGATGATCTTCACCAA	120		
QY	513	ATPATTTAGATCCAAACCAAGTTTATCAGAGATCAGTCTGACTGATCTGATATCAGCTC	572		
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QY	573	CTCGTGCCCTTAAATATACATCATTCGCGGATGTTCTTCATAGAGATCTCAAAACCGAG	632		
Db	181	CTTCGTGGGCTTAAGGATATATACATTTCTCCAAACATATCCATAGAGATTTGAAACCAAG	240		
QY	633	AACCTTTTGGTAAATGCAAAATTTGATCTTAAGATATGATGACTTTGGTCTTGAAGCCA	692		
Db	241	AACGCTGTTAAATATGCAAAATTTGACACTTGAAGATTTATGATTGGTCTTGGCCGACCA	300		
QY	693	AACATAGGAACGGAATATGACGAATATGTTGTAACACATGATGATGATGATGATGATG	752		
Db	301	ACTATGGAAGATGACTTTCATGACAGAAATATGTTGTCACGAATGATGATGATGATGATG	360		
QY	753	CTTTTGTGTAACCTCTTCGATTTACACTGCTCTATAGATGTTGGTCTGTCGTTGACATC	812		
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QY	813	TTTCATGGAACCTTATGAATAGAAAACCTTTGTTGGTGAAGAAAGATCATGATCAATATA	872		
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QY	873	CGCTTGTTAACCGAGCTCTTGTGACACCCACAGAGATGATCTTGGCTCTCCCAAAAT	932		
Db	481	CGCTTATTTAGACAGAGCTCTTGTGACACCTCCAACTGACGCTGATGTTGGGTTAGTAA	540		
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Db	541	GACGATGCGAAGATATATCCGACAACTCTCTCAGATTCCTCGTCAACCTTTGATAGG	600		
QY	993	GTTTTCCCTCATGGAACCAATTTGGCTTTGATCTTTCGATTAATAATTTGACATTTGAT	1052		
Db	601	GTITTCCTCCCATGTTTCATCTTACCAATGATCTTGTGATTAATAATTTGACATTTGAT	660		
QY	1053	CCTACTAGAGAATTTACAGTT 1073			
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LOCUS	AM775829	679 bp	mRNA	linear	EST 07-SEP-2000
DEFINITION	EST334894 DSIL Medicago truncatula cDNA clone pBSIL-3C6, mRNA				
ACCESSION	AM775829				
VERSION	AM775829.1	GI:7765642			
KEYWORDS	EST.				
ORGANISM	barrel medic.				
SOURCE	Medicago truncatula				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots;				
	Rosidae; eucotids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;				
	Medicago.				
	1 (bases 1 to 679)				
	Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng				

,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S.,
Holt,I.E. and Fraser,C.M.
ESTs from leaves of Medicago truncatula after inoculation with
Colletotrichum trifolii
Unpublished (2000)
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borling Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@puccini.crl.umn.edu
Minnesota sequence name: M259162X
TIGR sequence name: MTFALJ5TX
More information is available at:
http://chryslie.tamu.edu/medicago
Seq primer: Skmod (CTA gaa cta gta gat cc).
Location/Qualifiers

FEATURES

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/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pDSIL-3C6"
/clone_lib="DSIL"
/tissue_type="leaves infected with Colletotrichum
trifolii"
/dev_stage="cotyledons and primary leaves harvested 5 and
8 days after inoculation with Colletotrichum trifolii"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
cotyledons and primary leaves harvested 5 and 8 days after
inoculation with Colletotrichum trifolii. The cDNA was
directionally ligated into the uni-ZAP XR vector from
Stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells. Note: EST may
be of fungal origin."
BASE COUNT 198 a 137 c 133 g 211 t
ORIGIN

Query Match 26.0%; Score 449; DB 10; Length 679;
Best Local Similarity 79.2%; Pred. No. 1.9e-84;
Matches 533; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 399 CATTAGACCTGAAATGTAATGTTTGAAGACGATTCCTCCACCTTACGAAG 458
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DB 7 CATTAGATCATGAAATGTAATGTTTGAAGATGTTATCCACCACCTTGGTGA 66
QY 459 GAGTTTCTGATGTTACATGCTACTGACTGATGATGATGATGATGATGATG 518
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DB 67 GAGTTTATGATGTTTACATACCAACGACTGATGATGATGATGATGATGATG 126
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QY 519 AGATCAACCAAGGTTTATCAGAGATCAGTCACTTCACTTCACTTCACTTCC 578
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DB 127 CGCTCTAATCAAACTGTGATGAACACTGCAGTCTTTTGTATCAGATCTTCT 186
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QY 579 GGCTTAATATCATACATCTCCGCAATGTTTCTATAGAGATCTCAAAACGACACTT 638
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DB 187 GGGCTAAGATATATCATCTTGCACCAATATCATAGATTTGAAACCAAGCAACTG 246
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QY 639 TTGCTAATATGCAATTTGATCTTAAGATGATGATGATGATGATGATGATGAT 698
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DB 247 CTGTTAATATGCAATTTGATCTTAAGATGATGATGATGATGATGATGATGAT 306
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QY 699 GAGACGAGATATGACGGAATATGTTGTAACAGAGTACAGGACACAGAGCTTTTG 758
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DB 307 GAAAGTACTTCATGACAGATATGTTGTACAGAGATGATAGGGCTCTGAATTGTTG 366
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QY 759 TTGAAGTCTTCAGATTCACAGCTGCTATAGATGTTTGGTGTGCGTATCTCATG 818
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DB 367 TTGAAGTCTTCAGATTCACAGCTGCTATAGATGATGATGATGATGATGATGATG 426
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QY 819 GAAGTTATGATAGAAACCTTTGTTGGTGAAAAAGATCATGTCATCAATACGCTTG 878
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DB 427 GAGCTTATGAAATTAATAAACCTTCCTGTTCTGCAAGATCATGTCATCAATACGCTTGA 486
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QY 999 CCTCATGGAACCCATTTGGCTATGATCTTGGCTTAATAGTACATTCGATCTCACT 1058
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DB 607 CCCCATTGTCATCCCTGATGCAATTCATCTTGTGATTAATAAGTTGACAAATTCATCTAC 666
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QY 1059 AGAAGATTTACAG 1071
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DB 667 AGAAGATTTACAG 679
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RESULT 15
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LOCUS
DEFINITION NP016C05NR1P1000 Nodulated root Medicago truncatula cDNA clone
ACCESSION NP016C05NR 5', mRNA sequence.
VERSION AW684379
KEYWORDS AW684379.1 GI:7559115
SOURCE EST.
ORGANISM Medicago truncatula
barrel medic.

REFERENCE
AUTHORS Watson,B.S., Shu,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
Gonzales,R.A., Bell,C.J., Flores,H.R., Immen,J.T., Weller,J.W., May
,G.D. and Paiva,N.L.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula nodulated root library
Unpublished (2000)
Contact: Paiva NL
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7317
Fax: 580 221 7380
Email: nlpaiva@noble.org
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FEATURES

source

1. .672
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/clone="NF016C05NR"
/clone_lib="Nodulated root"
/tissue_type="root"
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a mixture of young and old roots and nodules."
BASE COUNT 186 a 123 c 148 g 212 t
ORIGIN

Query Match 25.9%; Score 447.2; DB 10; Length 672;
Best Local Similarity 80.2%; Pred. No. 4.5e-84;
Matches 535; Conservative 0; Mismatches 131; Indels 1; Gaps 1;
QY 254 GCGTATGCTGCTGCTTATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 313
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OY	374	TCTCCGTAGATTTAAGGCTCCGCCCATTTAGACCATGAATAGTAAATGGTTTAAGAGA	433
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OY	854	AGATCATATGATCAATAAATACGCTGTTTAAACGAGCTTCTTGGACCCCAACAGAAAGCTT	912
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Db	661	ATGTGGC 667	

GenCore version 5.1.5
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OM protein - protein search, using sw model

Run on: May 20, 2003, 00:23:42 ; Search time 54 Seconds

(without alignments)
669.797 Million cell updates/sec

Title: US-09-623-034-2

Perfect score: 1987
Sequence: 1 MADANMGAGGQFPDPFVS.....EQTKDMYQELSLNPEYA 375

Scoring table:

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Searched: 362588 seqs, 96450795 residues

Total number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1288	64.8	375	10	US-09-828-313-34 Sequence 34, Appl
2	885	44.5	624	9	US-10-072-036-57 Sequence 57, Appl
3	878.5	44.2	360	9	US-10-171-311-127 Sequence 127, App
4	877.5	44.2	604	9	US-10-072-036-59 Sequence 59, Appl
5	877.5	44.2	605	9	US-10-072-036-41 Sequence 41, Appl
6	868	43.7	353	10	US-09-801-368-116 Sequence 116, App
7	868	43.7	435	10	US-09-801-368-150 Sequence 150, App
8	867	43.6	379	9	US-10-059-585-37 Sequence 37, Appl
9	867	43.6	631	9	US-10-072-036-39 Sequence 39, Appl
10	846	42.6	360	9	US-09-918-873-35 Sequence 35, Appl
11	844	42.5	360	9	US-09-918-873-33 Sequence 33, Appl
12	842	42.4	360	9	US-09-918-873-34 Sequence 34, Appl
13	841	42.3	360	9	US-09-918-873-1 Sequence 1, Appl
14	838	42.2	606	9	US-10-072-036-65 Sequence 65, Appl
15	838	42.2	607	9	US-10-072-036-47 Sequence 47, Appl
16	837	42.1	360	9	US-09-918-873-32 Sequence 32, Appl
17	835	42.0	360	9	US-09-918-873-37 Sequence 37, Appl
18	833	41.9	360	9	US-09-918-873-38 Sequence 38, Appl
19	832	41.9	360	9	US-09-918-873-36 Sequence 36, Appl

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21	830	41.8	360	9	US-09-918-873-39	Sequence 39, Appl
22	829	41.7	360	9	US-09-918-873-26	Sequence 26, Appl
23	829	41.7	360	9	US-09-918-873-29	Sequence 29, Appl
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25	825	41.5	360	9	US-09-918-873-27	Sequence 27, Appl
26	825	41.5	360	9	US-09-918-873-28	Sequence 28, Appl
27	821	41.3	360	9	US-09-918-873-31	Sequence 31, Appl
28	819.5	41.2	364	9	US-10-198-343-2	Sequence 2, Appl
29	819.5	41.2	364	9	US-10-197-315-2	Sequence 178, App
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39	624.5	31.4	384	9	US-09-861-097-12	Sequence 12, Appl
40	624.5	31.4	384	9	US-09-861-098-12	Sequence 63, Appl
41	624.5	31.4	633	9	US-10-072-036-63	Sequence 45, Appl
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ALIGNMENTS

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RESULT 1
US-09-828-313-34
; Sequence 34, Application US/09828313
; Patent No. US20020059662A1
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSMALDO DA
; APPLICANT: BOHNER, HANS J
; APPLICANT: THELEN, NOCH VAN
; APPLICANT: CHEN, RODING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; FILE REFERENCE: 16313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 34
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-828-313-34

Query Match          64.8%  Score 1288; DB 10; Length 375;
Best Local Similarity 67.6%  Pred. No. 6.3e-101;
Matches 242; Conservative 46; Mismatches 68; Indels 2; Gaps 1;

OY 18 SVLTGGGYVDPDINGFETTKRPPIMPGRGAYGVSVLTELTENYAVKINA 77
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DB 14 SPTTGGHYKVVAGTPEVTARKKPLRPIGRKATIGVSLFTVTGEYAVKIGNA 73
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OY 78 FDIYDAKRTLEIKLRLHLDHENVIGLDVYIPPLRREFSDVYIATELMDTLQIIRS 137
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DB 74 FDNIRDAKRTLEIKLRLHMDHENVAITDIIRPTRENFNDVYIYVELMDTLQIIRS 133
| :|:| |:::|:| |:::|:|:| |:::|:| |:::|:| |
OY 138 NQGLSEDDCYFMYQLLGKTYHSANVLRDLKRSNLVYANCDLKTCDGLAPNEN 197
| :|:| |:::|:| |:::|:|:| |:::|:| |:::|:| |
DB 134 NQALTEHDICQYFLVQILGKTYHSANVLRDLKPTNLVYANCDLKTADGLATLTSET 193
| :|:| |:::|:| |:::|:|:| |:::|:| |:::|:| |
OY 198 EMTREYVTRMYRAPELLNSSDYPAADVWSVCCIPELMNRKPLFGCKDHVHQIRLLT 257
```

[illegible]

RESULT 2
 US-10-072-036-57
 : Sequence 57, Application US/10072036
 : Publication NO. US20030082564A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Ole THASTRUP
 : APPLICANT: Sara BJRON
 : APPLICANT: Soren TULLIN
 : APPLICANT: Kasper ALMHOLT
 : APPLICANT: Kurt SCUDDER
 :
 : TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To Ar
 : TITLE OF INVENTION: On A Cellular Response
 :
 : FILE REFERENCE: 3759-0120P
 :
 : CURRENT APPLICATION NUMBER: US/10/072,036
 :
 : CURRENT FILING DATE: 2002-09-13
 :
 : PRIOR APPLICATION NUMBER: 09/417,197
 :
 : PRIOR FILING DATE: 1999-10-07
 :
 : NUMBER OF SEQ ID NOS: 143
 :
 : SOFTWARE: PatentIn version 3.0
 :
 : SEQ ID NO 57
 :
 : LENGTH: 624
 :
 : TYPE: PRT
 :
 : ORGANISM: Artificial Sequence
 :
 : FEATURE:
 :
 : OTHER INFORMATION: MERK1-F64L-S65T-GFP fusion
 :
 : US-10-072-036-57

Query Match	44.58;	Score 885;	DB 9;	Length 624;
Best Local Similarity	46.38;	Pred. No. 1.3e-66;		
Matches 177; Conservative	72;	Mismatches 111;	Indels 22;	Gaps 7

```

OY 2 ADAMNAGGQ-----EPREPSVLNHGGYQDFJFGNFETITTKYRPIIMPICGAY 54
Db 4 AAAAPGGGGEPGCTAGYVPVPEVE-----VKGOPFDPRT-?OLOITGCAI 54
OY 55 GIVCSVLTELLENVAVAKIINAFEDIMADAKRTLRKILRHLNHDHENVIGLRDVIPEPLR 114
Db 55 GMVSSAYDHVAKTRAIKALI-SPEHQYTQCRTLREIQILIRFRHENVIGIRDLRAPTL 113
OY 115 REFSVYIATLMDTLHQITRSNOGLSEDBHQYFMQOLRGLKYHSANVNLHDLKPSN 174
Db 114 EAMRVYIYVOLMETDYLKLLKRSQ-LSNBHICFYVLQILRGKYHSANVNLHDLKPSN 172
OY 175 LLVANACDLKICDEGLAR---PNIENEN-MEYVVTWYRAPPELLNSSDYTAIDWVS 230
Db 173 LLINTCDLKCIDEGLARLADPEHDHGFLEIYATKRYAPPELMLSKGYSIDTWSV 222
OY 231 GCIFEMELMNRKPLFEGKGDHVHQIRLTELLEGTPTADLGFQONEDAKRYIROLPOHROQ 280
Db 233 GCILAEMLSNRPKIPGKHYLDQILNHLIGILGSPQEDLNCINMKKANYIQLSPSKRYA 292
OY 291 LAEVPHPVNLPLAIDLVDKMLTFEDPRTKRYVEALDHPYLAKLHADGDEPILCPVPESDFE 350
Db 293 WAKLFEPKSDSKALDLRLMLTFENPNKRITVEEALAHRYLEQYUYPDPEVAEEPEFDFME 352
OY 351 QQGIGEGEOIKDIMOALSLNP 372
Db 353 LDDPLKRLKELIFQETAPROP 374

```

RESULT 3

```

US-10-171-311-127
; Sequence 127, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangli
; APPLICANT: Glatz, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-127

```

Query Match	44.2%;	Score 878.5;	DB 9;	Length 360;
Best Local Similarity	48.6%;	Pred. No. 2.3e-6;		
Matches 168; Conservative	69;	Mismatches 102;	Indels 7;	Gaps 5;

Oy	33	GNEFFITKYPPLMPJGKGVYIVCSVLNLTENEMVAVKKIAAFIYDAKATTEIK	92
	16	GOVEDYGRY-TNLSYIGEGYMGVCSAYDNVKNVRAIKKI-SPEFHQYCCQTLREIK	73
Oy	93	ILRLHDEHNVIGLNDVLPPLRREPSDVIATLEMDITDLOIIRNSOGLEDHCQYMYQ	152
Db	74	ILLRREHNEIGIMDILRAPYIEOMKDYIVODIMETDLYKLAKT-OHLSNDHICPEYLO	132
Oy	153	ILRGKGYHSANVLRHDLKPSNLLVFNANCDKICDFGLAR--PNIENEN-MFEYVATRW	208
Db	133	ILRGKGYHSANVLRHDLKPSNLLNTTCDKICDFGLARADPDHHTGELFEYVATRW	192
Oy	209	YRABELLINSDDYRAADVMSVGCIFEMLNMRKPLFGCKDHVHOIRLTELGTPEADL	266
Db	193	YRAPETMINSNGYTKSIDIMWSGCIILAEMLSNRPJFQKHLNDLNLILGTSPOSEDL	252
Oy	269	GFLONEDAKRYIRQLPGHPRGOLAEVPHVAPLADLVDMKLLFDPDPIRIVTEALHPY	328
Db	253	NCIITLKNRNYLLSLPHKNKRYVMNRRLPNADSKALDLDLKLMTGTPNKRIRIEVEQALHPY	312
Oy	329	LAKLHDAGDEPICYPPSFDEOQIGEBQIKMDIITQEALSNEXY	374
Db	313	LEQYIDPSDEPIARPEFKFEMDLDLPEKKEIKELLEETARFOQY	358

RESULT 4
 US-10-072-036-59
 : Sequence 59, Application US/10072036
 : Publication No. US20030082564A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Ole THASTRUP
 : APPLICANT: Sara BJORN
 : APPLICANT: Soren TULLIN
 : APPLICANT: Kasper ALLMOLT
 : APPLICANT: Kurt SCUDDER
 :
 : TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To A
 : TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To A

```
FILE REFERENCE: 3759-0120P
: CURRENT APPLICATION NUMBER: US/10/072.036
: CURRENT FILING DATE: 2002-09-13
: PRIOR APPLICATION NUMBER: 09/417,197
: PRIOR FILING DATE: 1999-10-07
: NUMBER OF SEQ ID NOS: 143
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 59
: LENGTH: 604
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Efk2-EGFP fusion
US-10-072-036-59

Query Match          44.2%; Score 877.5; DB 9; Length 604;
Best Local Similarity 48.6%; Pred. No. 5.5e-66;
Matches 168; Conservative 69; Mismatches 102; Indels 7; Gaps 5;

QY 33 GNFETITKYPPIPIGRCAGYICSVLNTLNMVAVKRIANAFDIYMDAKRLREIK 92
D 14 GQVEDVGRY-TNLSTYIGGAYGWCASAYDNLNKRYVAIKKI-SPEEHOTYCQRLREIK 71
QY 93 LLRLDHEENVIGLRDVIPEPLRREFSDYIATLMDTDLHOIIRSNOCISEDHCOYFMQ 152
D 72 LLRRHRENIIGINDIIRAPTEIQMKDYIYQDLMETDLYKLKT-QHLSNDHICFYLQ 130
QY 153 LLRLGKYHSANVLRDLKPSNLVANCCLKICDFGLAR--PNIENEN-MTEYVVTM 208
D 131 ILRGLKYHSANVLRDLKPSNLVANCCLKICDFGLARVADPDHDTGFLTEYVATRM 190
QY 209 YRABELLNSDYTAIDVWSVGCIFMELMNRKPLFGCKDHVHQIRLLTELGTPTEDL 268
D 191 YRPEIMLNSKGYTSIDVWSVGCILAEMLNRPFPCKHYLDQNLHILIGISQEDL 250
QY 269 GFLONEDAKRYIROLPOHPRQOLAEVFPVNPPLAIDLVDKMLTFDPTRITVEALDHPY 328
D 251 NCIIILKARNYLSLPHKNKYPWNLFPNADSKALDLDKMLTFPHKRIEYEQALHPY 310
QY 329 LAKLHDAGDEPICVPFSEFEOGIGEOIKDMITYOEALSLNPEY 374
D 311 LEQYVDPSEPIAEAPFKFMDLDDLPRKELKELIFEETARQPGY 356

RESULT 5
US-10-072-036-41
: Sequence 41, Application US/10072036
: Publication No. US20030082564A1
: GENERAL INFORMATION:
: APPLICANT: Ole THASTRUP
: APPLICANT: Sara BJORN
: APPLICANT: Soren TULLIN
: APPLICANT: Kasper ALMHOLT
: APPLICANT: Kurt SCUDDER
: TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
: FILE REFERENCE: 3759-0120P
: CURRENT APPLICATION NUMBER: US/10/072.036
: CURRENT FILING DATE: 2002-09-13
: PRIOR APPLICATION NUMBER: 09/417,197
: PRIOR FILING DATE: 1999-10-07
: NUMBER OF SEQ ID NOS: 143
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 41
: LENGTH: 605
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: EGFP-Erk2 fusion
US-10-072-036-41

Query Match          44.2%; Score 877.5; DB 9; Length 605;
Best Local Similarity 48.6%; Pred. No. 5.5e-66;
```

```
Matches 168; Conservative 69; Mismatches 102; Indels 7; Gaps 5;

QY 33 GNFETITKYPPIPIGRCAGYICSVLNTLNMVAVKRIANAFDIYMDAKRLREIK 92
D 261 GQVEDVGRY-TNLSTYIGGAYGWCASAYDNLNKRYVAIKKI-SPEEHOTYCQRLREIK 318
QY 93 LLRLDHEENVIGLRDVIPEPLRREFSDYIATLMDTDLHOIIRSNOCISEDHCOYFMQ 152
D 319 LLRRHRENIIGINDIIRAPTEIQMKDYIYQDLMETDLYKLKT-QHLSNDHICFYLQ 377
QY 153 LLRLGKYHSANVLRDLKPSNLVANCCLKICDFGLAR--PNIENEN-MTEYVVTM 208
D 378 ILRGLKYHSANVLRDLKPSNLVANCCLKICDFGLARVADPDHDTGFLTEYVATRM 437
QY 209 YRABELLNSDYTAIDVWSVGCIFMELMNRKPLFGCKDHVHQIRLLTELGTPTEDL 268
D 438 YRPEIMLNSKGYTSIDVWSVGCILAEMLNRPFPCKHYLDQNLHILIGISQEDL 497
QY 269 GFLONEDAKRYIROLPOHPRQOLAEVFPVNPPLAIDLVDKMLTFDPTRITVEALDHPY 328
D 498 NCIIILKARNYLSLPHKNKYPWNLFPNADSKALDLDKMLTFPHKRIEYEQALHPY 557
QY 329 LAKLHDAGDEPICVPFSEFEOGIGEOIKDMITYOEALSLNPEY 374
D 558 LEQYVDPSEPIAEAPFKFMDLDDLPRKELKELIFEETARQPGY 603

RESULT 6
US-09-801-368-116
: Sequence 116, Application US/09801368
: Patent No. US20020128250A1
: GENERAL INFORMATION:
: APPLICANT: Busby, Robert
: APPLICANT: Call, Brian
: APPLICANT: Hecht, Peter
: APPLICANT: Holtzman, Doug
: APPLICANT: Madden, Kevin
: APPLICANT: Maxon, Mary
: APPLICANT: Milne, Todd
: APPLICANT: NO. US20020128250A1man, Thea
: APPLICANT: Royer, John
: APPLICANT: Salama, Sofie
: APPLICANT: Sherman, Amir
: APPLICANT: Silva, Jeff
: APPLICANT: Summers, Eric
: TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
: FILE REFERENCE: 109272.147
: CURRENT APPLICATION NUMBER: US/09/801.368
: CURRENT FILING DATE: 2001-03-07
: PRIOR APPLICATION NUMBER: US 09/487,558
: PRIOR FILING DATE: 2000-01-19
: PRIOR APPLICATION NUMBER: US 60/160,587
: PRIOR FILING DATE: 1999-10-20
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 116
: LENGTH: 353
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
US-09-801-368-116

Query Match          43.7%; Score 868; DB 10; Length 353;
Best Local Similarity 49.6%; Pred. No. 1.7e-65;
Matches 167; Conservative 61; Mismatches 91; Indels 18; Gaps 5;
```

```
QY 49 IGRGAYGICSVLNTLNMVAVKRIANAFDIYMDAKRLREIKLLRLDHEENVIGLRDVI 108
D 19 IGEAGYGVCSATHRKPTGEIYAIKKI-EPEKPLPALTRLREIKILKHKHENTITFINI 77
QY 109 IPPPLRREFSDYIATLMDTDLHOIIRSNOCISEDHCOYFMQILRLGKYHSANVLR 168
D 78 QRPDSFENFENYIIQELMQTDLHRYI-STQMLSDHIOYFIYQRLRAVKVYLAGSNVIR 136
```

QY 169 DLKPSNLLVANCNDLKICDFGLAR-----PNIENEMTEYVTRWRAPPELLN 217
DB 137 DLKPSNLLVANCNDLKICDFGLARIDESADNSEPTEGOSGMTYVTRWRAPPELLT 196
QY 218 SSDTALIDVWSVGCIFMELNKRPLFGKDHVQIIRLLTGLTP-TEADLGSLQWEDA 276
DB 197 SAKYSRAMDVWSCGIIAEFLRRPIFGDRYRQLLITGIICTPSDNDLRCSIESPA 256
QY 277 KRYIRQLPQHPROQLAEVPHVNPALIDLVDKMLTFDPTRRIIVTEALDHPYAKLADAG 336
DB 257 REYIKSLPMPAPALEMFPVRNPKGIDILQRMVFPDPAKRITAKELAEHYIOTYIDPN 316
QY 337 D---EPICVPESFDFEQGIGEEQIKDMYOPALS 369
DB 317 DEPEGEPIPSFEFEDHYKEALTTKDLKILWNEIFS 353

RESULT 7
US-09-801-368-150
; Sequence 150, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Call, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 150
; LENGTH: 435
; TYPE: PRF
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-150

Query Match 43.7%; Score 868; DB 10; Length 435;
Best Local Similarity 46.9%; Pred. No. 2.3e-65;
Matches 165; Conservative 68; Mismatches 111; Indels 8; Gaps 4;
QY 20 LTHGGOYVQEDIRGNFEITTKYRPPIMPICRGAYGIVCSYVLTNLEMAVAKKIANAFD 79
DB 1 MTNEEPIRQIFGTVEITNRYN-DLNPVGMGAFGLVCSATDILTSQPAVKIMPFSS 59
QY 80 IYMDAKRTLEIKLRHLDHENVIGLRDVIPPPLRRESDVIYATLEIMDDTDLHOIIRSNQ 139
DB 60 TAYLAKRTYELKLLKLRHLENLCLQDIFLSP-----EDITYTELQGDTHRLQDT-R 114
QY 140 GLSEDHCOYEMYQOLLRLGLKYIHSANVLRDLKPSNLLVANCNDLKICDFGLARPNINEN 199
DB 115 PLEKQFQYVQLYQIRGLKAYHSAGYVIRHDLKPSNLLINENCDLKICDFGLAR--IQDPQ 172
QY 200 MTEYVTRWRAPPELLNNSDYTAIDVWSVGCIFMELNKRPLFGKDHVQIIRLLTEL 259
DB 173 MTGVSTRYRRAPIMLTWQKYDEVEDVWSGICFAEMIEGKPLFGKDHVQHSITDL 232
QY 260 LGPTEADLGSLQWEDAKRYIRQLPQHPROQLAEVPHVNPALIDLVDKMLTFDPTRIT 319

DB 233 LGSPKDVINTICSENTLKFVTSILPHRDPIPFSSERFTEBDAVDLLEKMLVEDPKRIT 292
QY 320 VEALDHPYAKLADAGDEPICVPFSEFDEQGIGEEQIKDMYOPALSIN 371
DB 293 AADALAPYSPYHDPTEPVDADAKFDMHFNDAIDPDTMRVMMYSILLDFH 344

RESULT 8
US-10-059-585-37
; Sequence 37, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 379
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-059-585-37

Query Match 43.6%; Score 867; DB 9; Length 379;
Best Local Similarity 45.8%; Pred. No. 2.3e-65;
Matches 175; Conservative 71; Mismatches 114; Indels 22; Gaps 7;
QY 2 ADANMGAGGCG-----FPDPFSVLTGCGYVDFIFGNFEITTKYRPPIMPICRGAY 54
DB 3 AAAAGGGGCGEPRTGEGVGPVEVM-----VKGQPFVGPYR-TOLYIGGAY 53
QY 55 GIVCSYVLTNLEMAVAKKIANAFDIYMDAKRTLEIKLRHLDHENVIGLRDVIPPPLR 114
DB 54 GWSASAVDHRKTRVAAIKKI-SPEHQTTCORTIREIQLIRFHHENVIGIRDLRASTL 112
QY 115 REESDYIATLEIMDDTDLHOIIRSNQGLSEDHCOYEMYQOLLRLGLKYIHSANVLRDLKPSN 174
DB 113 EAMNDVIYIYQDLMETDYLKLLKSSQ-LSNDHICVFLYQIRGLKYIHSANVLRDLKPSN 171
QY 175 LTVANCNDLKICDFGLAR-----PNIENEMTEYVTRWRAPPELLNNSDYTAIDVWSV 230
DB 172 LSNWTDLKLICDFGLARIDPEHDHGFLEVYVATRWYRAPEIMLSKSGYTSIDIMSY 231
QY 231 GCIFMELNKRPLFGKDHVQIIRLLTGLTPTEADLGSLQWEDAKRYIRQLPQHPROQ 290

Db 232 GCILAEMLSNRPIFGKHYLDOLNHLIGLSPQEDLNCIMMKARNYLQSLPSTKTA 291
QY 291 LAEVPHPVPLAIDLVDKMLTDPTRRTIVEEALDHPYLAKLHADDEPICPPSPESFDE 350
Db 292 WAKLFPKSSKALDLDRLMTFENPKRRTIVEEALHPYLEQYVDPDEPAEPEPFAME 351
QY 351 OOGIGEOKIMYOEALSLNP 372
Db 352 LDDLPKRLKEILFOETARFOP 373

RESULT 9
US-10-072-036-39

; Sequence 39, Application US/10072036
; Publication No. US20030082564A1
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP
; APPLICANT: Sara BJORN
; APPLICANT: Soren TULLIN
; APPLICANT: Kasper ALMHOLT
; APPLICANT: Kuit SCUDDER
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0120P
; CURRENT APPLICATION NUMBER: US/10/072,036
; CURRENT FILING DATE: 2002-09-13
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: EGFP-Erk1 fusion construct
US-10-072-036-39

Query Match

Best Local Similarity 45.8%; Score 867; DB 9; Length 631;
Matches 175; Conservative 71; Mismatches 114; Indels 22; Gaps 7;

QY 2 ADANMGAGGQ-----PPDESVYLTGCGYVQFDIFGNFETTKYRPPIMIGRGAY 54
Db 255 AAAAGGGGGGRRRTGCVGPVGEVEM-----VKQPPDVGRY-TQLQYIEGAY 305
QY 55 GIVCSVLTNLEMDVAVKKIANAFDIYMDAKRTLEIKLLRLDHEENVGLRDVPPPLR 114
Db 306 GWSSAYDHVTRKTRVAIKKI-SPEHQYTCORTLEIQILRLRPHENVIGRIDILASTL 364
QY 115 REFSVYITELMDDDLHOIIRSNOCGLSDHCYFMYQLLRGLKTYHSANVLRDLKPSN 174
Db 365 EAMRDVYIYQDLMETDLYKLKLSQO-LSNDHICYFLYQILRGKTYHSANVLRDLKPSN 423
QY 175 LTVNANCDLKICDFGLAR---PNIENEN-MTEYVYTRWRAPPELLNSSDYRAAIDVWGV 230
Db 424 LLSNTTCDLKICDFGLARLADPEHDTGTLTEYVATRWRAPEIMLNSGYTKSIDIWVY 483
QY 231 GCIFELMNRKPLFGSGKHVQIRLLTTELLGTPTEADLGFLONEADAKRYIRQLPQHPROO 290
Db 484 GCILAEMLSNRPIFGKHYLDOLNHLIGLSPQEDLNCIMMKARNYLQSLPSTKTA 543
QY 291 LAEVPHPVPLAIDLVDKMLTDPTRRTIVEEALDHPYLAKLHADDEPICPPSPESFDE 350
Db 544 WAKLFPKSSKALDLDRLMTFENPKRRTIVEEALHPYLEQYVDPDEPAEPEPFAME 603
QY 351 OOGIGEOKIMYOEALSLNP 372
Db 604 LDDLPKRLKEILFOETARFOP 625

RESULT 10
US-09-918-873-35

; Sequence 35, Application US/09918873
; Publication No. US20030032649A1
; GENERAL INFORMATION:
; APPLICANT: Goldsmith, Elizabeth J.
; APPLICANT: Radna, Akella
; APPLICANT: Gaynor, Richard B.
; TITLE OF INVENTION: CHIMERIZING PROTEIN KINASES FOR DRUG
; FILE REFERENCE: A33864 090495.0232
; CURRENT APPLICATION NUMBER: US/09/918,873
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: GSK-3/p38 inhibitor binding site chimera
US-09-918-873-35

Query Match

Best Local Similarity 42.6%; Score 846; DB 9; Length 360;
Matches 163; Conservative 65; Mismatches 107; Indels 6; Gaps 5;

QY 36 FETTTYRPPIMIGRAGIVCSYVTELENEVAVKRIANARDIYMDAKRTIREIKLR 95
Db 18 WEYPERYQ-NLSPVGGAGSVCAAFDTKGHRVAVKKSRRPQSIHAKRYRELRLK 76
QY 96 HDHENVIGLRDVIYPPPLR-REFSDVYITELMDTDLHOIIRSNOCGLSDHCYFMYQLL 154
Db 77 HMDHCNVIGLDVYTPARSLSEPNVYLVYDLMGADLNTVKC-QULTDQVGFLLYQIL 135
QY 155 RGLKTYHSANVLRDLKPSNLVYANCDLKICDFGLARPIENENMTEYVYTRWRAPEL 214
Db 136 RGLKTYHSADIIHRDLKPSNLAVNEDECELDLDFGLARHT--DDEMTGYATRWRAPEI 193
QY 215 LNSSDYTAIDVWSVGCIFELMNRKPLFGGDHVOIRLLTTELLGTPTEADLGLONE 274
Db 194 LNMWNYNOTVDIWSVGCIMAEELLTGTLEPGTDHIDQLIRLVTGPQAEILLKISS 253
QY 275 DAKRYIRQLPQHPROOLAEVFPHPVPLAIDLVDKMLTDPTRRTIVEEALDHPYLAKLHD 334
Db 254 SARNTYISLAQMKMFANVFICANPLAYDLLEKMLYVDSKRTTAQALAHAFQYHD 313
QY 335 AGDEPICVPFSPFEQOGIGEOKIMYOEALSLNPEYA 375
Db 314 PDDEPVAD-PYDQSFESRDLIDEMKSLTYDEVISFVPPHA 353

RESULT 11

US-09-918-873-34
; Sequence 34, Application US/09918873
; Publication No. US20030032649A1
; GENERAL INFORMATION:
; APPLICANT: Goldsmith, Elizabeth J.
; APPLICANT: Radna, Akella
; APPLICANT: Gaynor, Richard B.
; TITLE OF INVENTION: CHIMERIZING PROTEIN KINASES FOR DRUG
; FILE REFERENCE: A33864 090495.0232
; CURRENT APPLICATION NUMBER: US/09/918,873
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: JNK-3/p38 inhibitor binding site chimera
US-09-918-873-34

[illegible]

```

RESULT 12
US-09-918-873-33
: Sequence 33, Application US/09918873
: Publication No. US20030032649A1
GENERAL INFORMATION:
APPLICANT: Goldsmith, Elizabeth J.
APPLICANT: Radna, Akella
TITLE OF INVENTION: CHIMERIZING PROTEIN KINASES FOR DRUG
TITLE OF INVENTION: DISCOVERY
FILE REFERENCE: A33864 090495.0232
CURRENT APPLICATION NUMBER: US/09/918,873
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 360
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: MEK1/p38 inhibitor binding site chimera
US-09-918-873-33

```

	Query Match	Similarity	42.4%	Score 842;	DB 9;	Length 360;
	Best Local	Similarity	47.5%	Pred. No. 2,8e-63;		
	Matches	162;	Conservative	65;	Mismatches 108;	Indels 6; Gaps 5;
QY	36	FEITTKYRPPIICRGAGIVCSVLTELNMVAVKKIAPNAFDIYMDAKRTLEIKLIR	95			
Db	18	WVPERVQ-NLSPVSGAGVSCAAFDKGTGRVAVPKKLSRPFOSIIHAKKRYREIRLLK	76			
QY	96	HLIDHENVIGLRVYIPPLR-REFSVYUATLMDVDLHIIISNOGLSDHCQYFMYQL	154			
Db	77	HHNHNVIGLDFPPARSLSEEFNDVYLVTILMGADLNNIYVC-OKLDDHVFLLYQL	135			
QY	155	RGKLIHSAANVLHRLDKPSNLLVNAACDKLIDCFGLARPIENENMTEYVYTRWYRAPEL	214			
Db	136	RGKLIHSAADLIHRLDKPSNLLVNAEDCEKLIDFGLARHT--DDEMTGVAATRWYRAPEI	193			
QY	215	LINSSDYNAIDVWVSGCFEMELNMRKPLPGSGKDHYHOIRLLTELLGFTPEADLGEIONE	274			
Db	194	MLNMHHYQVYDIMSVCIMAEILLGRLPLFPTDHIHQLLIRLVGPRGAEALLKISSE	253			
QY	275	DAKRYIROLPHPRQOLAEVFPNVBLAIDLVDKKILGFDTPRRTITVEEALDHPYLAUKLMD	334			

```
Db      254 SAKRNTQSLAOMPKNFANVFATIGANPLAVDLLEKMLVIDSRKTAAQAALAHAFYQH D   31.3  
Oy      335 AGDEPICVPFPSEDFEEGGIGEIKDMIVYOALSINPEVA    375  
            ||| : | : | : : | : | : | : | :  
Db      314 PDDEFVAD-PYDQSFSERDLLIDEMKSLTVDYEVSFPTHA    353  
  
RESULT 13  
US-09-g18-873-1  
; Sequence 1, Application US/069918873  
; Publication No. US20030032649AI  
; GENERAL INFORMATION:  
; APPLICANT: Goldsmith, Elizabeth J.  
; APPLICANT: Radha, Akella  
; APPLICANT: Gaynor, Richard B.  
; TITLE OF INVENTION: CHIMERIZING PROTEIN KINASES FOR DRUG  
; FILE REFERENCE: A33864 090495_0232  
; CURRENT APPLICATION NUMBER: US/09/g18, 873  
; CURRENT FILING DATE: 2002-07-31  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-g18-873-1
```

Query Match	Similarity	42.3%	Score	84	DB	9	Length	360
Best Local	47.9%	Pred.	No.	3	4e-63			
Matches	162	Conservative	63	Mismatches	107	Indels	6	Gaps
Qy	36	FEITTKYRPPIMPIGRCAGYIVCSVLTNLEMYAVKKIANAEIYDAKRTLEIKLR	95					
Db	18	WEVERPY-NISPYSGAGYSCAFDPTKHTRAVVKLSRPFOSIIHAKRTYELIKL	76					
Qy	96	HLDHENYVGLRDYVPPRLR-REFSVYATLMTDILHOIIRSNQGLSEBHCQFWMQL	154					
Db	77	HMKHENYVGLDVFPPASLEEFNDYVLYTHIMADLNNIYC-QRLTDHYQFLYQIL	135					
Qy	155	RGKLIHSANYLHRLDKPSNLVYANACDLKICDFGLRPNTEENMETEYVYTRAPRL	214					
Db	136	RGKLIHSADIIHRLKPSNLAVNDEDLKILDFGLARHT--DEEMGYATRTYRAPEI	193					
Qy	215	LINSDDYAAADIVMSVGCIFMELNNRKPLFCGKHVHOIRITFLTEGLTPREADIGFLONE	274					
Db	194	MINMHYIOTYVDINSVCSIMAEELLGRLTFPGTHIDQLKILRVSTPGKALLKRSSE	253					
Qy	275	DAKRIYIQLPQHPRQQLAEVFRPHVPLAIDLVDKMLTFDPTRITVEBALDHPYLAKLD	334					
Db	254	SARNTISLAMPKKNFANVETIGANPLAVDLEKMLIDSKRTTAQALAHVFAADYH	313					

```

; RESULT 14
; US-10-072-036-65
; Sequence 65, Application US/10072036
; Publication No. US20030082564A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Ole THASTRUP
;
; APPLICANT: Sara BJORN
;
; APPLICANT: Soren TULLIN
;
; APPLICANT: Kasper ALMHOLT
;
; APPLICANT: Kurt SCUDDER
;
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To A
; TITLE OF INVENTION: On A Cellular Response
; FILE REFERENCE: 3759-0120P
; CURRENT APPLICATION NUMBER: US/10/072.036
; CURRENT FILING DATE: 2002-09-13
;

```

```

; PRIOR APPLICATION NUMBER: 09/417,197
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p38-EGFP fusion
US-10-072-036-65

```

```

Query Match          42.2%; Score 838; DB 9; Length 606;
Best Local Similarity 47.9%; Pred. No. 1.2e-62;
Matches 162; Conservative 63; Mismatches 107; Indels 6; Gaps 5;

```

```

QY 36 FEITTKYRPPIMPIGGAGIVCSVLNTELMNMAVAKKIAPFDIYMDAKRTLRREIKILR 95
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 WEVPERYQ-NLSPVSGAAGSYCAAFDRTGLRVAVKKISRPFQSIHAKRTYRELRLIK 76
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 96 HLDHENVIGLRDVIPTPLR-REFSDVYIATELMDTDLHOIISNOCGLSDHCQYFMYQL 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 77 HKKHENVIGLRDVIPTPLR-REFSDVYIATELMDTDLHOIISNOCGLSDHCQYFMYQL 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 155 RGLKTIHSANVLHRLDKPSNLLVNAACDLKICDFGLARPINENMTEVYTRWYRAPEL 214
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 RGLKTIHSADIIHRLDKPSNLLVNAACDLKICDFGLARPINENMTEVYTRWYRAPEL 193
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 215 LINSDDYTAIDVWSVGCIFMELMNKRPFGSKDHVHOIRLTTELGTPTTEADLGFIONE 274
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 194 MLNMMHYNOTVDIWSVGCIMAEELTGRITFPGTDHIDQLILRLVGTGAEELKKISSE 253
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 275 DAKRYIROLPOHPRQOLAEVFPVHNPALIDVDMKLTPTTRRIYVEALDHPYLAKLHD 334
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 254 SARNTIOSLTQMPKMFANVFIGNAPLAVDLLEKMLVLDSDKRITPAQALAHAYFAQYHD 313
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 335 AGDEPICVPFSPDFEEOGIGEOIKDMYQEALSLNP 372
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 314 PDDEPVAD-PYDOSFESRDLIDEMKSLTYDEVISFVP 350
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 15
US-10-072-036-47
; Sequence 47, Application US/10072036
; Publication No. US20030082564A1
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP
; APPLICANT: Sara BJORN
; APPLICANT: Soren TULLIN
; APPLICANT: Kasper ALMHOLT
; APPLICANT: Kurt SCUDDER
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
; FILE REFERENCE: 3759-0120P
; CURRENT APPLICATION NUMBER: US/10/072,036
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/417,197
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EGFP-p38 fusion
US-10-072-036-47

```

```

Query Match          42.2%; Score 838; DB 9; Length 607;
Best Local Similarity 47.9%; Pred. No. 1.2e-62;
Matches 162; Conservative 63; Mismatches 107; Indels 6; Gaps 5;

```

```

QY 36 FEITTKYRPPIMPIGGAGIVCSVLNTELMNMAVAKKIAPFDIYMDAKRTLRREIKILR 95

```

```

Db 265 WEVPERYQ-NLSPVSGAAGSYCAAFDRTGLRVAVKKISRPFQSIHAKRTYRELRLIK 323
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 96 HLDHENVIGLRDVIPTPLR-REFSDVYIATELMDTDLHOIISNOCGLSDHCQYFMYQL 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 324 HKKHENVIGLRDVIPTPLR-REFSDVYIATELMDTDLHOIISNOCGLSDHCQYFMYQL 382
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 155 RGLKTIHSANVLHRLDKPSNLLVNAACDLKICDFGLARPINENMTEVYTRWYRAPEL 214
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 383 RGLKTIHSADIIHRLDKPSNLLVNAACDLKICDFGLARPINENMTEVYTRWYRAPEL 440
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 215 LINSDDYTAIDVWSVGCIFMELMNKRPFGSKDHVHOIRLTTELGTPTTEADLGFIONE 274
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 441 MLNMMHYNOTVDIWSVGCIMAEELTGRITFPGTDHIDQLILRLVGTGAEELKKISSE 500
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 275 DAKRYIROLPOHPRQOLAEVFPVHNPALIDVDMKLTPTTRRIYVEALDHPYLAKLHD 334
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 501 SARNTIOSLTQMPKMFANVFIGNAPLAVDLLEKMLVLDSDKRITPAQALAHAYFAQYHD 560
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 335 AGDEPICVPFSPDFEEOGIGEOIKDMYQEALSLNP 372
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 561 PDDEPVAD-PYDOSFESRDLIDEMKSLTYDEVISFVP 597
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Search completed: May 20, 2003, 00:31:55
Job time : 56 secs

```


GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2003, 00:16:27 ; Search time 43 Seconds
(without alignments)
838.382 Million cell updates/sec

Title: US-09-623-034-2
Perfect score: 1987
Sequence: 1 MADANMAGAGGQFPDPSPVL.....EEQIKDMITGEALSLNPEYA 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1987	100.0	375	2 T03971	mitogen-activated
2	1662	83.6	370	2 T47504	mitogen-activated
3	1661	83.6	370	2 S40469	mitogen-activated
4	1650	83.0	371	2 T14915	mitogen-activated
5	1634	82.2	371	2 T09622	protein kinase MMK
6	1509	75.9	393	2 S51321	mitogen-activated
7	1500.5	75.5	387	2 S48123	mitogen-activated
8	1498.5	75.4	394	2 S33635	mitogen-activated
9	1498.5	75.4	395	2 S40472	mitogen-activated
10	1473	74.1	369	2 S56638	mitogen-activated
11	1340.5	67.5	376	2 S40470	mitogen-activated
12	1308	65.8	371	2 S60121	mitogen-activated
13	1292	65.0	371	2 S51320	mitogen-activated
14	1285	64.7	363	2 C86214	hypothetical prote
15	1279.5	64.4	393	2 T47803	mitogen-activated
16	1274	64.1	376	2 S40471	mitogen-activated
17	1258.5	63.1	369	2 C86146	hypothetical prote
18	1244.5	62.6	373	2 T13024	probable protein x
19	1219	61.3	406	2 D84898	mitogen-activated
20	1094.5	55.1	372	2 S39559	mitogen-activated
21	1078	54.3	370	2 F86236	protein F14N23.9
22	1075.5	54.1	384	2 S52989	mitogen-activated
23	1069	53.8	376	2 F96619	MAP kinase (ATMPK7
24	1061	53.4	368	2 B84561	MAP kinase (ATMPK7
25	1052	52.9	368	2 S40473	mitogen-activated
26	1029.5	51.8	415	2 A56042	mitogen-activated
27	1002	50.4	361	2 C85430	MAP kinase like pr
28	924	46.5	356	2 T51944	pathogenicity MAP
29	900.5	45.3	361	2 T51943	mitogen-activated

30	896.5	45.1	376	2 A36978	MAP kinase mpk-1 (
31	896.5	45.1	444	2 A36977	MAP kinase sur-1 (
32	885	44.5	377	2 S28184	Ca2+/calmodulin-de
33	884.5	44.5	369	2 JW0053	extracellular sign
34	883	44.4	380	2 JC1451	Ca2+/calmodulin-de
35	879	44.2	392	2 JW0052	extracellular sign
36	878.5	44.2	360	1 J01400	MAP kinase 1 (EC 2
37	878	44.2	815	2 B56708	extracellular sign
38	877.5	44.2	358	2 S16444	mitogen-activated
39	877.5	44.2	358	2 A40033	protein kinase (EC
40	877.5	44.2	360	2 S25011	protein kinase ERK
41	877.5	44.2	369	2 A60041	Ca2+/calmodulin-de
42	875	44.0	349	2 S68675	mitogen-activated
43	872	43.9	372	2 S15663	protein kinase (EC
44	871.5	43.9	361	2 A3754	mitogen-activated
45	868	43.7	353	2 S28548	protein kinase (EC

ALIGNMENTS

RESULT 1

T03971
mitogen-activated protein kinase (EC 2.7.1.-) WIPK - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000
C:Accession: T03971
R:Seq. S.: Okamoto, M.; Seto, H.; Ishizuka, K.; Sano, H.; Ohashi, Y.
Science 270, 1988-1992, 1995
A:Title: Tobacco MAP kinase: a possible mediator in wound signal transduction pathway
A:Reference number: 215170; MUID:96123271; PMID:8533090
A:Accession: T03971
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-375 <SEO>
A:Cross-References: EMBL:D61377; NID:g1136297; PIDN:BAA09600.1; PID:g1136298
C:Comment: MAP kinase is part of the initial response of higher plants to mechanical
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:40-329/Domain: protein kinase homology <KIN>

Query Match 100.0%; Score 1987; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 9.7e-89;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MADANMAGAGGQFPDPSPVLTHGGQYVQFDIFGNFFETTKYRPPIPIGRGAYGIVCSV	60
DB	1	MADANMAGAGGQFPDPSPVLTHGGQYVQFDIFGNFFETTKYRPPIPIGRGAYGIVCSV	60
QY	61	LNTELNEMVAVKKINAPDIYMDAKRTLEIKLRLHDEHYIGLRDVIPLPLRRFSNV	120
DB	61	LNTELNEMVAVKKINAPDIYMDAKRTLEIKLRLHDEHYIGLRDVIPLPLRRFSNV	120
QY	121	YATLEMDTDLHQIIRSNGLSEDCQYPMYOLLRLGKTYHSANVYLRDLKSNLNVNAN	180
DB	121	YATLEMDTDLHQIIRSNGLSEDCQYPMYOLLRLGKTYHSANVYLRDLKSNLNVNAN	180
QY	181	CDLKICDEGLAPNLENEMTEYVVTWYRAPELLNNSDYPAADVWSGCIPELMNR	240
DB	181	CDLKICDEGLAPNLENEMTEYVVTWYRAPELLNNSDYPAADVWSGCIPELMNR	240
QY	241	KPLFGSKDHVHDIRLTLLGTPTLADLGEFLQNEAKRYIRLOLPOHROOLAEVPHVNP	300
DB	241	KPLFGSKDHVHDIRLTLLGTPTLADLGEFLQNEAKRYIRLOLPOHROOLAEVPHVNP	300
QY	301	LAIDLVDKMLTFDPTTRITVEEALDHPYLAKLHDAAGDEICVPSFDEQOGIGEEQIK	360
DB	301	LAIDLVDKMLTFDPTTRITVEEALDHPYLAKLHDAAGDEICVPSFDEQOGIGEEQIK	360
QY	361	DMITGEALSLNPEYA 375	
DB	361	DMITGEALSLNPEYA 375	

RESULT 2
T47504

mitogen-activated protein kinase 3 - Arabidopsis thaliana

N:Alternate names: protein F9K21.220

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence, revision 20-Apr-2000 #text, change 19-May-2000

Accession: T47504

R:Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K. submitted to the Protein Sequence Database, February 2000

A:Reference number: 224467

A:Accession: T47504

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-370 <J0R>

A:Cross-references: EMBL:AL138657

A:Experimental source: cultivar Columbia; BAC clone F9K21

C:Genetics:

A:Map position: 3

A:Insertions: 53/2; 96/3; 142/3; 253/3; 315/1

A:Note: F9K21.220

C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 83.6%; Score 1662; DB 2; Length 370;
Best Local Similarity 82.4%; Pred. No. 3.5e-73;
Matches 304; Conservative 36; Mismatches 29; Indels 0; Gaps 0;

QY 6 MGAGGQPPDPSPVLTGCGYVDFGPFETTKYRPPIMPGRGAYGVCVLTNEL 65

Db 1 MNTGGQYTDPRPAVETHGQFISYDIFGSLFEITSKYRPIPIGRGAYGVCVLTNET 60

QY 66 NEMVAKKIANAFDIYMDAKRTLEIKLRHLHDHENYIGLDVIPPRLRFSVYATL 125

Db 61 NELVAMKKIANAFNMHMDAKRTLEIKLRHLHDHENIYAIIDVPPRLRFSVYISTE 120

QY 126 LMDTDLHQIIRSNOSLSEHCQYFLYQLRGLKTYHSANVLRDLKPSNLLNANCDLKI 185

Db 121 LMDTDLHQIIRSNOSLSEHCQYFLYQLRGLKTYHSANVLRDLKPSNLLNANCDLKI 180

QY 186 CDFGLARPENENMTETVYTRWYRAPPELLNNSDYTAIDVWSYGCIFMELMNRKPLFG 245

Db 181 CDFGLARPTSENDPMTETVYTRWYRAPPELLNNSDYTAIDVWSYGCIFMELMNRKPLFP 240

QY 246 GKDHVQIRLTTELIGTPTTEADLGFLOVEDAKRYTRQLPQHPROQLAEVPHVNPALD 305

Db 241 GKDHVQIRLTTELIGTPTTESDLGFTNEDAKRYTRQLPQHPROPLAKLFGHVPMALD 300

QY 306 VDKMLTDPPTRRITVEALDHPYLAKLHDADDEPFCVPFSGFDEQOIGSEQIKMDIYQ 365

Db 301 VDKMLTDPPTRRITVEALDHPYLAKLHDADDEPFCVPFSGFDEQOIGSEQIKMDIYQ 360

QY 366 EALSINPEY 374

Db 361 EALINLPTY 369

RESULT 3

S40469

mitogen-activated protein kinase 3 (EC 2.7.1.-) - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 06-Oct-1994 #sequence, revision 19-Jan-1996 #text, change 20-Jun-2000

C:Accession: S40469

R:Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.

FEBS Lett. 336, 440-444, 1993

A:Title: ATPKs: a gene family of plant MAP kinases in Arabidopsis thaliana.

A:Reference number: S40469; MUID:94109583; PMID:8282107

A:Accession: S40469

A:Molecule type: mRNA

A:Residues: 1-370 <MIZ>

A:Cross-references: EMBL:DJ1839; NID:9457397; PIDN:BA04866.1; PID:9457398

C:Genetics:

A:Gene: MPK3

C:Superfamily: kinase-related transforming protein; protein kinase homology

C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:35-324/Domain: protein kinase homology <KIN>
F:44-52/Region: protein kinase ATP-binding motifQuery Match 83.6%; Score 1661; DB 2; Length 370;
Best Local Similarity 82.4%; Pred. No. 3.9e-73;
Matches 304; Conservative 36; Mismatches 29; Indels 0; Gaps 0;

QY 6 MGAGGQPPDPSPVLTGCGYVDFGPFETTKYRPPIMPGRGAYGVCVLTNEL 65

Db 1 MNTGGQYTDPRPAVETHGQFISYDIFGSLFEITSKYRPIPIGRGAYGVCVLTNET 60

QY 66 NEMVAKKIANAFDIYMDAKRTLEIKLRHLHDHENYIGLDVIPPRLRFSVYATL 125

Db 61 NELVAMKKIANAFNMHMDAKRTLEIKLRHLHDHENIYAIIDVPPRLRFSVYISTE 120

QY 126 LMDTDLHQIIRSNOSLSEHCQYFLYQLRGLKTYHSANVLRDLKPSNLLNANCDLKI 185

Db 121 LMDTDLHQIIRSNOSLSEHCQYFLYQLRGLKTYHSANVLRDLKPSNLLNANCDLKI 180

QY 186 CDFGLARPENENMTETVYTRWYRAPPELLNNSDYTAIDVWSYGCIFMELMNRKPLFG 245

Db 181 CDFGLARPTSENDPMTETVYTRWYRAPPELLNNSDYTAIDVWSYGCIFMELMNRKPLFP 240

QY 246 GKDHVQIRLTTELIGTPTTEADLGFLOVEDAKRYTRQLPQHPROQLAEVPHVNPALD 305

Db 241 GKDHVQIRLTTELIGTPTTESDLGFTNEDAKRYTRQLPQHPROPLAKLFGHVPMALD 300

QY 306 VDKMLTDPPTRRITVEALDHPYLAKLHDADDEPFCVPFSGFDEQOIGSEQIKMDIYQ 365

Db 301 VDKMLTDPPTRRITVEALDHPYLAKLHDADDEPFCVPFSGFDEQOIGSEQIKMDIYQ 360

QY 366 EALSINPEY 374

Db 361 EALINLPTY 369

RESULT 4

T14915

mitogen-activated protein kinase I (EC 2.7.1.-) - parsley

N:Alternate names: MAP kinase I

C:Species: Petroselinum crispum (parsley)

C:Date: 20-Sep-1999 #sequence, revision 20-Sep-1999 #text, change 21-Jul-2000

C:Accession: T14915

R:Ligterink, W.; Kroj, T.; zur Nieden, U.; Hirt, H.; Scheel, D.

Science 276, 2054-2057, 1997

A:Title: Receptor-mediated activation of a MAP kinase in pathogen defense of plants.

A:Reference number: 218265; MUID:97342856; PMID:9197271

A:Accession: T14915

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-371 <LIG>

A:Cross-references: EMBL:Y12785; NID:92231033; PIDN:CAA7323.1; PID:92231034

C:Comment: MAP kinase is part of the initial response of higher plants to mechanical

C:Superfamily: kinase-related transforming protein; protein kinase homology

C:Keywords: ATP; phosphotransferase

F:36-325/Domain: protein kinase homology <KIN>

Query Match 83.0%; Score 1650; DB 2; Length 371;
Best Local Similarity 81.7%; Pred. No. 1.3e-72;
Matches 300; Conservative 39; Mismatches 28; Indels 0; Gaps 0;

QY 9 GGAGQPPDPSPVLTGCGYVDFGPFETTKYRPPIMPGRGAYGVCVLTNELNM 68

Db 5 GDGQYTDPRPAVETHGQFISYDIFGSLFEITSKYRPIPIGRGAYGVCVLTNETNM 64

QY 69 VAVKIANAFDIYMDAKRTLEIKLRHLHDHENYIGLDVIPPRLRFSVYATLMD 128

Db 65 VAVKIANAFDIYMDAKRTLEIKLRHLHDHENYIATIDVIPPRLRFSVYATLMD 124

QY 129 TDLHQIIRSNOSLSEHCQYFLYQLRGLKTYHSANVLRDLKPSNLLNANCDLKI 188

Db 125 TDLHQIIRSNOSLSEHCQYFLYQLRGLKTYHSANVLRDLKPSNLLNANCDLKI 184

Db 190 LKPSNLLNANCDLKICDGLARVTSESDFMTEYVTRWYRAPPELLNNSDYTAIDVMS 249
QY 230 VCCIEFELMNRKPLFGKDHVHOIRLTTELLGPTREADIGFLQNEADAKRYTROLPOHPRQ 289
Db 250 VCGIFELMDKRPFLPGKHVHQLRLMELIGPSEEELEFL-NEAKKRIKRLPPYRQ 308
QY 290 QLAIEVPHVNPALIDLVDMLTFDPRTTVEBALDHPYAKLHDAGDPIPCVPPSPF 349
Db 309 SITDKRPYVHPLAIDLIEKMLTFDPRRRRTIVDALAHPLNLSHDSDEPCTIRPNPDE 368
QY 350 EOOGIGEEOIKDVIYOALSLNPEY 374
Db 369 ENHALSEEQMKELIYREALAFNPEY 393

RESULT 10

S56638
mitogen-activated protein kinase 1 homolog (clone AspK9) - oat
N:Alternate names: MAP1 kinase
C:Species: Avena sativa (oat)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 18-Jun-1999
C:Accession: S56638
R:Huttlly, A.K.; Phillips, A.L.
Plant Mol. Biol. 27, 1043-1052, 1995
A>Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that show
A:Reference number: S56638; MUID:95284341; PMID:7766874
A:Accession: S56638
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-369 <HUT>
A:Cross-references: EMBL:X79993; NID:g871983; PIDN:CAA56314.1; PID:g871984
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase; protein kinase
F:33-322/Domain: protein kinase homology <KIN>
F:42-50/Region: protein kinase ATP-binding motif

Query Match 74.1%; Score 1473; DB 2; Length 369;
Best Local Similarity 72.9%; Pred. No. 4e-64;
Matches 266; Conservative 52; Mismatches 47; Indels 0; Gaps 0;

QY 10 GGOFDPFVYLTHGQYVDFGDFEITTKYRPPIMPICRGAYIVCSVLNTELEMY 69
Db 3 GAPVAEFPTMTHGGFLLYNIFGNOFELTSKYQRPIMPICRGAYIVCSVMNFTREMY 62
QY 70 AKKIANAFDIYMDAKRTLRKILRLHLDHENYIGLDVIYPPRLREFSDVYATLMDT 129
Db 63 AKKIANAFDIYMDAKRTLRKILRLHLDHENYIGLDVIYPPRLREFSDVYATLMDT 122
QY 130 DLHQIIRSNQGLSEDHCOYFMQLGLKTYHSANVLRDLKPSNLLVANCDLKICDGL 189
Db 123 DLHIIIRSNQGLSEDHCOYFMQLGLKTYHSANVLRDLKPSNLLVANCDLKICDGL 182
QY 190 LARPNTENMTYVTRRYRAPPELLNNSDYTAIDVMSVGCIFMELNMRKPLFGKDH 249
Db 183 LARPNTENMTYVTRRYRAPPELLNNSDYTAIDVMSVGCIFMELNMRKPLFGKDH 242
QY 250 VHOIRLTTELLGPTREADIGFLQNEADAKRYTROLPOHQAOLAEVPHVNPALIDLVDMA 309
Db 243 MHQMRITLIVETIGTPDDDLGFLINEDAKRYKMLHLPFRPPRPGQPKYQPALDLIERK 302
QY 310 LTFDPTRTVEBALDHPYAKLHDAGDPIPCVPPSPFEOOGIGEEOIKDVIYOALS 369
Db 303 LTFNPLORTVEBALDHPYAKLHDAGDPIPCVPPSPFEOOGIGEEOIKDVIYOALS 362
QY 370 LNPEY 374
Db 363 LNPNE 367

RESULT 11

S40470
mitogen-activated protein kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana
N:Alternate names: MAP kinase

C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 06-Oct-1994 #sequence_revision 19-Jan-1996 #text_change 03-May-2002
C:Accession: S40470 #sequence_revision 19-Jan-1996 #text_change 03-May-2002
R:Minoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 336, 440-444, 1993
A>Title: ATPKs: a gene family of plant MAP kinases in Arabidopsis thaliana.
A:Reference number: S40469; MUID:94109583; PMID:8282107
A:Accession: S40470
A:Molecule type: mRNA

A:Residues: 1-376 <MIN>
A:Cross-references: EMBL:D21840; NID:g457399; PIDN:BA04867.1; PID:g457400
R:Schmitt, P.; Magg, L.
Submitted to the EMBL Data Library, June 1997

A:Description: The sequence of A. thaliana IG002N01.
A:Reference number: 214407

A:Accession: T01707

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-40, 'N', 59-147, 153-312, 'D', 314-376 <SCH>

A:Cross-references: EMBL:AF007269; NID:g2191126; PIDN:AMB61033.1; PID:g2191146
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp

Nature 402, 769-777, 1999
A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A:Reference number: AB5001; MUID:20083488; PMID:10617198
A:Accession: H85017

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-312, 'D', 314-376 <STO>

A:Cross-references: GB:NC_001268; NID:g7267634; PIDN:CAB80946.1; GSPDB:GN00140
C:Genetics:

A:Gene: MPK4; AT4901370

A:Map position: 4

A:introns: 41/2; 101/3; 147/3; 258/3; 320/1

C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F:40-329/Domain: protein kinase homology <KIN>
F:49-57/Region: protein kinase ATP-binding motif

Query Match 67.5%; Score 1340.5; DB 2; Length 376;
Best Local Similarity 65.1%; Pred. No. 8.9e-58;
Matches 242; Conservative 64; Mismatches 65; Indels 1; Gaps 1;

QY 2 ADANMGAGGQPPFVYLTHGQYVDFGDFEITTKYRPPIMPICRGAYIVCSVL 61
Db 3 ADECFSSDDQ-SSSKGVATHGSSVQYVYVGLFVSKYPPPLRIGRGAYICATP 61
QY 62 NTELNMAVAVKTIANAFDIYMDAKRTLRKILRLHLDHENYIGLDVIYPPRLREFSDVY 121
Db 62 NSETGEVAIKKIGNAFDNIIDAKRTLRKILRLHLDHENYIAVKDIIRPQRENENDVY 121
QY 122 IATELMDTDLHQTIRSNQGLSEDHCOYFMQLGLKTYHSANVLRDLKPSNLLVANAG 181
Db 122 IATELMDTDLHQTIRSNQGLSEDHCOYFMQLGLKTYHSANVLRDLKPSNLLVANAG 181
QY 182 DLKICDGLARVTSESDFMTEYVTRWYRAPPELLNNSDYTAIDVMSVGCIFMELNMRK 241
Db 182 DLKICDGLARVTSESDFMTEYVTRWYRAPPELLNNSDYTAIDVMSVGCIFMELNMRK 241
QY 242 PLFGGDHVOIRLTTELLGPTREADIGFLQNEADAKRYTROLPOHQAOLAEVPHVNPAL 301
Db 242 PLFGGDHVOIRLTTELLGPTREADIGFLQNEADAKRYTROLPOHQAOLAEVPHVNPAL 301
QY 302 AIDLVKMLTFDPTRTTVEBALDHPYAKLHDAGDPIPCVPPSPFEOOGIGEEOIKD 361
Db 302 AIDLVKMLTFDPTRTTVEBALDHPYAKLHDAGDPIPCVPPSPFEOOGIGEEOIKD 361
QY 362 MIYOALSLNPE 373
Db 362 LTYRETVKFNPDQ 373

RESULT 12

S60121

Db 129 QTLTDHCQFLYQILRGKITYHSANVLHRDLKPSNLVLTNDCLKICDFGLARTSENETE 188
QY 199 NMTEVYVFWYRAPPELLNSSDYTAIDWWSGCIFFMELMNRKPLFGKDNHQIRLLPE 258
Db 189 IMTEYVVRWYRAPPELLNSSSEYTAIDWWSGCIFFMELTRETLEFPKDYVOQLKITE 248
QY 259 LIGTPTTEADLGFIONEDAKRYTROLPOHPRQOLAEVFPVNPPLAIDLVDKMLTFDPTTRI 318
Db 249 LIGSPDDSDLDPLRSDNARKYKQLPHVOKOSFREKFPNISPMALDLAEKMLVFDPISKRI 308
QY 319 TVEEALDHPYLAKLHDAGDEPICVPVFPSPFEOGIGEBQIKDMITYQAL 368
Db 309 TVDEALKQPYLASHINEEPTCPFPSPFETALDPODIKELVWRESL 358

RESULT 15

T47803
mitogen-activated protein kinase-like protein - Arabidopsis thaliana
N:Alternate names: protein F24G16.60
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: T47803
R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, February 2000
A:Reference number: 224477
A:Accession: T47803
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-393 <DAN>
A:Cross-references: EMBL:AL138647
A:Experimental source: cultivar Columbia; BAC clone F24G16
C:Genetics:
A:Map position: 3
A:Introns: 75/2; 118/3; 164/3; 275/3; 336/1
A:Note: F24G16.60
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 64.4%; Score 1279.5; DB 2; Length 393;
Best Local Similarity 66.3%; Pred. No. 7.8e-55;

Matches 238; Conservative 51; Mismatches 69; Indels 1; Gaps 1;

QY 15 DPPSVLTHGGQYVQDFDIFGNFETTKYRPIPIPIGAGYGVCSVLTNLENNMVAVKKI 74
Db 32 DIPGTLSDHGRYIQYNLFCHIFELPAKYKPIPIPIRGACGIVCSAVDSETNKVAIKKI 91
QY 75 ANAFDIYMDAKRTLEIKILRLHLDHENVIGLDVYIPPLRREPSDVIYATELMDTDLHQI 134
Db 92 TQVFNPTLEAKRTLEIKILRLHFDHENIYAIRDVIILPQORDSFEDVIYINELMEFDLYRT 151
QY 135 IRSNGLSHSDHCQYFMYQLLRGLKITYHSANVLHRDLKPSNLVLTNDCLKICDFGLARP 194
Db 152 LKSDDELTKDHGMFYQILRGKITYHSANVLHRDLKPSNLVLTNDCLKICDFGLARAT 211
QY 195 IENENKTEVYVTRWYRAPPELLNSSDYTAIDWWSGCIFFMELMNRKPLFGKDNHQIR 254
Db 212 PESNLMTEVYVTRWYRAPPELLNSSDYTAIDWWSGCIFFMELMNRKPLFGKDNHQIR 271
QY 255 LTELIGTPTTEADLGFIONEDAKRYTROLPOHPRQOLAEVFPVNPPLAIDLVDKMLTFDP 314
Db 272 LLELELIGTPTTEADLGFIONEDAKRYTROLPOHPRQOLAEVFPVNPPLAIDLVDKMLTFDP 330
QY 315 TRRITVEEALDHPYLAKLHDAGDEPICVPVFPSPFEOGIGEBQIKDMITYQALSLNPE 373
Db 331 KORISVKEALAHPLYSFHDITDEPCSPFNFDLDEHPFSEQFRELITYCEALAFNPE 389

Search completed: May 20, 2003, 00:24:29
Job time : 44 secs

GenCore version 5.1.5
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OM protein - protein search, using sw model

Run on: May 19, 2003, 23:01:26 ; Search time 37 Seconds

(without alignments)
420.368 Million cell updates/sec

Title: US-09-623-034-2

Sequence: 1 MADANMGAGGCGFPDPFVS.....EQIKDMITQGLSLNPEYA 375

Scoring table:

BIOSUM62
Gap0 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1662	83.6	370	1	MPK3_ARATH
2	1509	75.9	393	1	NTF4_TOBAC
3	1500.5	75.5	387	1	MMK1_MEDSA
4	1498.5	75.4	394	1	MAPK_PEA
5	1498.5	75.4	395	1	MPK6_ARATH
6	1344.5	67.7	376	1	MPK4_ARATH
7	1312	66.0	371	1	MMK2_MEDSA
8	1292	65.0	371	1	NTF6_TOBAC
9	1284	64.6	376	1	MPK5_ARATH
10	1094.5	55.1	372	1	NTF3_TOBAC
11	1078	54.3	370	1	MPK1_ARATH
12	1075.5	54.1	384	1	MAPK_PETHY
13	1069	53.8	376	1	MPK2_ARATH
14	1061	53.4	368	1	MPK7_ARATH
15	1038.5	52.3	415	1	ERK1_DICDI
16	896.5	45.1	444	1	SUR1_CAEEL
17	883	44.4	380	1	MK03_RAT
18	878.5	44.2	360	1	MK01_HUMAN
19	878	44.2	806	1	MK07_MOUSE
20	878	44.2	815	1	MK07_HUMAN
21	877.5	44.2	358	1	MK01_MOUSE
22	877.5	44.2	360	1	MK01_BOVIN
23	877.5	44.2	361	1	MK01_XENLA
24	875	44.0	349	1	STYL_SCHPO
25	872	43.9	372	1	SPK1_SCHPO
26	872	43.9	379	1	MK03_HUMAN
27	868	43.7	353	1	FUS3_YEAST
28	868	43.5	435	1	HOG1_YEAST
29	864.5	43.4	365	1	M14B_DROME
30	862.5	43.0	376	1	ERKA_DROME
31	854	43.0	417	1	ERK1_CANAL
32	850.5	42.8	366	1	M14A_DROME
33	846	42.6	361	1	MK14_CYPCA

34	845.5	42.6	377	1	HOG1_CANAL	O92207 candida alb
35	841	42.3	360	1	MK14_MOUSE	P47811 mus musculu
36	839	42.2	360	1	MK14_RAT	P70618 rattus norv
37	838	42.2	360	1	MK14_HUMAN	O16539 h mitogen-a
38	837	42.1	422	1	SPM1_SCHPO	O92398 schizosacch
39	836	42.1	360	1	MK14_CANPA	O02812 canis famli
40	831.5	41.8	314	1	MK03_MOUSE	O63844 m mitogen-a
41	830	41.8	361	1	MK14_XENLA	P47812 xenopus lae
42	828.5	41.7	484	1	SLT2_YEAST	O00772 saccharomyc
43	824	41.5	501	1	MK01_CANAL	P43068 candida alb
44	807.5	40.6	364	1	MK11_MOUSE	O9wu11 mus musculu
45	806.5	40.6	372	1	MK11_HUMAN	Q15759 homo sapien

ALIGNMENTS

RESULT 1

MPK3_ARATH STANDARD: PRT: 370 AA.

AC O39023; Q9M1B3;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mitogen-activated protein kinase homolog 3 (EC 2.7.1.-) (MAP kinase 3)
DE (AEMPK3).
GN MPK3 OR AT3G45640 OR FPK21.220 OR T6D9.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=94109583; PubMed=8282107;
RA Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,
RA Shinozaki K.,
RT "AtMPKs: a gene family of plant MAP kinases in Arabidopsis thaliana";
RL FEBS Lett. 336:440-444(1993).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unsel M.,
RA Fatmann B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,
RA DeSimone M., Boutry M., Griwell L.A., Maché R., Puigdomenech P.,
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brotlier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wummbach E., Drzonek H., Effle H., Jordan N., Bangerter S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nykatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchenin D.,
RA Cooke R., Laudie M., Berger-Liauro C., Purnelle B., Masny D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A.C., Casacubeta E.,
RA Monfort A., Argilou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,
RA Cready T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Miltischer J., Sellers P., Gill J.E., Feldlyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana.";
RL Nature 408:820-822(2000).

```

RN [3]
RC SEQUENCE FROM N.A.
RP STRAIN-CV. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Riken Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SSP consortium (Salk/Stanford/PGSC).";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D21839; BAA04866.1; -
DR EMBL; AL138657; CAB75493.1; -
DR EMBL; AL157735; -; NOT_ANNOTATED_CDS.
DR EMBL; AF386961; AAK62406.1; -
DR HSSP; Q16539; 1WEC.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003527; MAP_kin.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Prodom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS01351; MARK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KM Phosphorylation; Multigene family.
FT DOMAIN 38 324 PROTEIN KINASE.
FT NP_BIND 44 52 ATP (BY SIMILARITY).
FT BINDING 67 67 ATP (BY SIMILARITY).
FT ACT_SITE 164 164 BY SIMILARITY.
FT MOD_RES 196 196 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 198 198 (BY SIMILARITY).
FT MOD_RES 198 198 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT CONFLICT 15 15 E -> D (IN REF. 1).
SQ SEQUENCE 370 AA; 42716 MW; 6992A7D97F3C9841 CRC64;
Query Match 83.6%; Score 1662; DB 1; Length 370;
Best Local Similarity 82.4%; Pred. No. 2.2e-101;
Matches 304; Conservative 36; Mismatches 29; Indels 0; Gaps 0;
QY 6 MGAGGGPPPPSVLTGNGQYQDFDGFNGFEITTKYRPPIMP1GRCAGYGVSVLNTL 65
DB 1 MNTGGGQYTPDPNAVETHGGQFISYDIFGSLFEITSKRYRPIIP1GRAGYGVSVLDIET 60
QY 66 NEMAVAKKINAFPIYDAAKTRLEIKLRHLHDEHNYIGLDVPIPP1LRREFSVYATE 125
DB 61 NEIYAMAKKINAFNDHDAKTRLEIKLRHLHDEHNYIAIDVYPP1LRQFSVYISTE 120
QY 126 LMDTDLHQTIRSNQSLSDHCQYFMQYQLRLGLKTYHSANVHLRLKSNLLVYANCDLKI 185
DB 121 LMDTDLHQTIRSNQSLSDHCQYFLYQLRLGLKTYHSANVHLRLKSNLLVYANCDLKI 180
QY 186 CDFGLARPNIENEMTEVYVTRWRAPPELLNSSDYTAIDVMSVGCIFMELANRRKPLFG 245
DB 181 CDFGLARPNIENEMTEVYVTRWRAPPELLNSSDYTAIDVMSVGCIFMELANRRKPLFP 240
QY 246 GKDHVHOIRLTTELGLPTTEADLGFLONEAKKRYIRQLPOHPRQOOLAEVPHVNP1ALD 305
DB 241 GKDHVHOIRLTTELGLPTTESDLGFTHNEDAKRYIRQLPNEPRQPLAKLIFSHVNP1ALD 300
QY 306 VDKMLTFDPTRRIVEALDHPYIAKLHDAGDEP1CVPFSPFDEQGIQGEQIKDMITQ 365

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DB 301 VDRMLTFDPNRRITVEQALNHQYLAKLHDPNDEPICQPFSEFEQOPLDEQIKEMITQ 360
QY 366 EALSINPEY 374
DB 361 EALINPEY 369
RESULT 2
NTF4_TOBAC STANDARD; PRT; 393 AA.
ID NTF4_TOBAC
AC Q40532;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitogen-activated protein kinase homolog NTF4 (EC 2.7.1.-) (P45).
GN NTF4.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_Taxid=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. Petit Havana SRI.
RX MEDLINE=96061956; PubMed=7586752.
RA Wilson C., Anglmayer R., Vicente O., Heberle-Bors E.;
RT "Molecular cloning, functional expression in Escherichia coli, and
RT characterization of multiple mitogen-activated-protein kinases from
RT tobacco";
RL Eur. J. Biochem. 233:249-257(1995).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC -1- PHOSPHORYLATION (BY SIMILARITY).
CC -1- PTM: VERY LOW AUTOPHOSPHORYLATION, ALTHOUGH DRAMATICALLY INCREASED
CC WHEN MN2+ IS ADDED TO THE REACTION INSTEAD OF MG2+.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL; X83880; CAA58761.1; -
DR HSSP; P27703; 1ERK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003527; MAP_kin.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Prodom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS01351; MARK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KM Phosphorylation; Multigene family.
FT DOMAIN 60 345 PROTEIN KINASE.
FT NP_BIND 66 74 ATP (BY SIMILARITY).
FT BINDING 89 89 ATP (BY SIMILARITY).
FT ACT_SITE 186 186 BY SIMILARITY.
FT MOD_RES 218 218 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 220 220 (BY SIMILARITY).
FT MOD_RES 220 220 PHOSPHORYLATION (ACTIVATES THE KINASE)
SQ SEQUENCE 393 AA; 45119 MW; 76EC1F3B1F174AB9 CRC64;
Query Match 75.9%; Score 1509; DB 1; Length 393;
Best Local Similarity 72.6%; Pred. No. 2.1e-91;
Matches 278; Conservative 44; Mismatches 49; Indels 12; Gaps 2;

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QY      3  DANNAGGCGGP-----DFPSVLTHGQVYQFDFISNFEITTKRTPRIMPIGR  51
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      9  DTVMASDAQGPAPPSPQVAGIDINIPATLSHGSRFLQYVIFGNIFEVYAKKPIIMPIGK  68
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      52  GATGVCVSLNLTENEMVAVKIYANFDIYMAKRTIREIKLRHLDHENVIGLGDVYRP  111
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      69  GATGVCVSLNLTENEMVAIKKIYANFPDKIDAKRTIREIKLRHMDHENVYALIDTIYRP  128
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      112  PLRREFSDVYIATELMDTDLHQIIRSNQGLSEDHCOYFYOLLRLGKYIHSANVLAHDLK  171
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      129  PQREAFNDVYIAYELMDTDLHQIIRSNQGLSEEHQGFLYQLRLGKXIYHSANVLAHDLK  188
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      172  PSNLLVANCDLKIICDFGLARPMIENENMTEYVYTRWYTAPELLNSSDYTAIDVWSYG  231
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      189  PSNLLNANCDLKIICDFGLARVTSFENDPMTEYVYTWYTAPELLNSSDYTAIDVWSYG  248
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      232  CIFMELNMRKPLFCGKQHVQIRLTTELGTPTFADLGLQEDNKKRYIRQLPQHRQOL  291
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      249  CIFMELNMRKPLFCGRHVQIRLTLLELTGTPTFADLGLQEDNKKRYIRQLPQHRQOL  307
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      292  AEVFPVHNPALADLVDMKLTFFDTPRRITVEEALDHPYIAKLHDADGDEPICVPSFDFEQ  351
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      308  VEKFPVHNPALADLVDMKLTFFDPRRRITYEDALHPYILSLDIDSDEPCVMCFNFDFEQ  367
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      352  QGIGEEQDKMITQVEALSNPEY  374
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      368  HALTEEQMKELTYREGIATNPEY  390
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

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ID	MMKL_MEDSA	STANDARD:	PRT:	387 AA.
AC	007176:			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	01-OCT-1994 (Rel. 30, Last sequence update)			
DT	30-MAY-2000 (Rel. 38, Last annotation update)			
DE	MITOGEN-activated protein kinase homolog MMKL (EC 2.7.1.-) (MAP kinase MSK7) (MAP kinase ERK1).			
GN	MMKL OR MSK7 OR ERK1.			
OS	Medicago sativa (Alfalfa).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae;			
OC	eucosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.			
OX	NCBI_TaxID=3879;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Embryo;			
RX	MEDLINE=94035163; Pubmed=8220466;			
RA	Jonak C., Pay A., Boegre L., Hirt H., Heberle-Bors E.;			
RT	"The plant homologue of MAP kinase is expressed in a cell cycle-			
RL	dependent and organ-specific manner.";			
RL	Plant J. 3:611-617(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Iroquois; TISSUE=Seedling root;			
RX	MEDLINE=93177216; Pubmed=8439746;			
RA	Duerer B., Gawlenowski M., Ropp T., Jacobs T.;			
RT	"MEERK: a mitogen-activated protein kinase from a flowering plant.";			
RL	Plant Cell 5:87-96(1993).			
CC	-1- FUNCTION: MAY PLAY A ROLE IN THE MITOGENIC INDUCTION OF SYMBIOTIC			
CC	ROOT NODULES ON ALFALFA BY RHIZOBIUM SIGNAL MOLECULES.			
CC	-1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE			
CC	PHOSPHORYLATION (BY SIMILARITY).			
CC	-1- TISSUE SPECIFICITY: ROOTS AND STEMS.			
CC	-1- PTM: AUTOPHOSPHORYLATED.			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	MAP KINASE SUBFAMILY.			
CC	-----			
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CC or send an email to license@isb-sib.ch).

DR	InterPro: IPR0000719; Euk_kinase.
DR	InterPro: IPR003527; MAP_kin.
DR	InterPro: IPR002290; ser_thr_Pkinase.
DR	Pfam: PF00069; Pkinase_1.
DR	ProDom: PDD000001; Euk_Pkinase; 1.
DR	SMART; SMO0220; S_TKc; 1.
DR	ProSite; PS01351; MAPK; 1.
DR	ProSite; PS00107; PROTEIN_KINASE_ATP; 1.
DR	ProSite; PS50011; PROTEIN_KINASE_DOM; 1.
DR	ProSite; PS00108; PROTEIN_KINASE_ST; 1.
KW	Transferase; Serine/threonine-protein kinase; ATP-binding;
KW	Mitosis; Cell cycle; Conjugation; Phosphorylation.
FT	DOMAIN 55 340 PROTEIN_KINASE.
FT	NP_BIND 61 69 ATP (BY SIMILARITY).
FT	BINDING 84 84 ATP (BY SIMILARITY).
FT	ACT_SITE 181 181 BY SIMILARITY.
FT	MOD_RES 213 213 PHOSPHORYLATION (ACTIVATES THE KINASE) (BY SIMILARITY).
FT	MOD_RES 215 215 PHOSPHORYLATION (ACTIVATES THE KINASE).
SO	SEQUENCE 387 AA; 44401 MW; 8672871AD34EAD2 CRC64;

Query Match	75.58;	Score 1500.5;	DB 1;	Length 387;
Best Local Similarity	74.38;	Pred. No. 7.3e-91;		
Matches 278; Conservative	43;	Mismatches 52;	Indels 1;	Gaps 1;

[illegible]

KM Phosphorylation: Multigene family.
 FT DOMAIN 63 348 PROTEIN KINASE.
 FT NP_BIND 69 77 ATP (BY SIMILARITY).
 FT BINDING 92 92 ATP (BY SIMILARITY).
 FT ACT_SITE 189 189 BY SIMILARITY.
 FT MOD_RES 221 221 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT (BY SIMILARITY).
 FT MOD_RES 223 223 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT (BY SIMILARITY).
 SQ SEQUENCE 395 AA; 45057 MW; 296D2BD7536DD4 CRC64;
 (BY SIMILARITY).
 Query Match 75.4%; Score 1498.5; DB 1; Length 395;
 Best Local Similarity 71.4%; Pred. No. 1e-90;
 Matches 275; Conservative 49; Mismatches 48; Indels 13; Gaps 2;
 QY 2 ADANMGAGGQFP-----DEPSVLTGCGQYQDPIDFENFEITTKYRPIMPI 49
 DB 10 ADPEMTAPGGFPAAPSPQMPGIENTPATLSHGCRFQYQYMFQNFIEVTAKKPPIMPI 69
 QY 50 GRGAYGVCSVLTENLNMVAVKRIANAFDIYMDAKRLRITKLRLHDHENVGLRDVI 109
 DB 70 GKRGAYGVCSAMNSETESVAIKKIANAFDNKIDAKRLRITKLRLHDHENVGLRDVI 129
 QY 110 PPLRLREFSDVYIATLMDTDLHQIIRSNQSLSDHCQYFMYQLRGLKTHSANVLRHD 169
 DB 130 PPLRLNAPFNDVYIATLMDTDLHQIIRSNQSLSDHCQYFMYQLRGLKTHSANVLRHD 189
 QY 170 LKPSNLLVANCCLKICDFGLARPNINENNTVEYVTRWYAPPELLNSSDYTAIDWMS 229
 DB 190 LKPSNLLVANCCLKICDFGLARPNINENNTVEYVTRWYAPPELLNSSDYTAIDWMS 249
 QY 230 VGCIFMELMNRKPLFGSKDHYHQIRLTLLGTPTEDLGLQMEDAKRYRQIPQHRQ 289
 DB 250 VGCIFMELMNRKPLFGSKDHYHQIRLTLLGTPTEDLGLQMEDAKRYRQIPQHRQ 308
 QY 290 QLAQVFPVNPPLAIDLYDKMTFPTPTRTIYEALDHPYAKLHDAGDEPTCPVPFSEDF 349
 DB 309 SLDKFPFTVPLAIDLIEKMTLPDRRRTITVIALAPHYLSLHDISEPCTTIPFNFDF 368
 QY 350 EQQIGEEQIRKDMIOEALSLNPEY 374
 DB 369 ENHALSEQKELITREALAFNPEY 393
 RESULT 6
 MPK4_ARATH STANDARD; PRT; 376 AA.
 ID MPK4_ARATH STANDARD; PRT; 376 AA.
 AC Q39024; Q9M136; O04597;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitogen-activated protein kinase homolog 4 (EC 2.7.1.-) (MAP kinase 4)
 DE (AtMPK4).
 GN MPK4 OR ATG601370 OR F2N1.1 OR F2N1-2-t.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=94109583; PubMed=8282107;
 RA Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,
 RA Shinozaki K.;
 RT "AtMPKs: a gene family of plant MAP kinases in Arabidopsis thaliana";
 RL FEBS Lett. 336:440-444(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083448; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,

RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
 RA Kreis M., Deiseny M., Puigdomenech P., Watson M., Schmidtmann T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hobeisel J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schuren J., Grymonprez B., Chiang Y.-J., Vandenbussche F.,
 RA Braeken M., Weljens I., Voet M., Bastiaens J., Aert R., Defoor E.,
 RA Weitzenecker T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
 RA Holzner E., Brandt A., Peters S., van Staveren M., Dirkse W.,
 RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Benneiser S., Hempel S., Feldpausch M., Lambrecht S., Van den Daele H.,
 RA De Keyser A., Buyschaert C., Gijlen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
 RA Petlet A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borkova D., Bloeker H., Scharfe M., Grimm M., Lochert T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fatmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Argüello A., Vitale D., Liguori R., Pivardelli E.,
 RA Massenot O., Quigley F., Clabaud G., Muenlein A., Felber R.,
 RA Schindl S., Hiller R., Berger C., Monfort A., Casacuberta E.,
 RA Clefidor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Glibons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacón D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bielke C.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Panelli L., Dedhia N., Gnoj L., Schütz K., Huang E., Spiegel L.,
 RA Sakhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Hartom G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Pulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Giesel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antonolli B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekhar M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
 RA Granat S., Shohdy N., Hasegawa A., Rodriguez M., Hoffman J., Tili S.,
 RA Chen E., Marra M., Martienssen R., McComble W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana";
 RL Nature 402:769-777(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Riken Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SSP consortium (Salk/Stanford/GCSC).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THRONINE
 PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE SUBFAMILY.
 CC -1- CAUTION: Ref. 2 (AA61033) sequence differs from that shown due
 CC to erroneous gene model prediction.
 CC
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 CC
 CC EMBL: D21840; BAA04867.1; -;
 CC EMBL: AL161491; CAB80946.1; -;
 CC EMBL: AF007269; AAB61033.1; ALT_SEQ.
 CC EMBL: AF360231; AAK25941.1; -;
 CC EMBL: AY040031; AAK64089.1; -;
 CC HSSP: Q16539; IWFC.
 CC InterPro: IPR000719; Euk_pkinase.


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ID NTF6_TOBAC STANDARD: PRT: 371 AA.
AC Q40531.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitogen-activated protein kinase homolog NTF6 (EC 2.7.1.-) (P43).
GN NTF6.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OC NCB1_TaxID=4097;
RN NCB1
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Petit Havana SRI;
RX MEDLINE=96061956; PubMed=7588752;
RA Wilson C., Anglimayer R., Vicente O., Heberle-Bors E.;
RT "Molecular cloning, functional expression in Escherichia coli, and
RT characterization of multiple mitogen-activated-protein kinases from
RT tobacco."
RL Eur. J. Biochem. 233:249-257(1995).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- PTM: VERY LOW AUTOPHOSPHORYLATION, ALTHOUGH DRAMATICALLY INCREASED
CC WHEN MN2+ IS ADDED TO THE REACTION INSTEAD OF MG2+.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X83879; CAAS8760.1; -
DR HSSP: Q16539; IMFC.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003527; MAP_Kin.
DR InterPro: IPR002290; Ser_thr_Pkinase.
DR Pfam: PF00068; Pkinase; 1.
DR ProDom: PD000001; Euk_Pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Multigene family.
FT DOMAIN 38 324 PROTEIN KINASE.
FT NP_BIND 44 52 ATP (BY SIMILARITY).
FT BINDING 67 67 ATP (BY SIMILARITY).
FT ACT_SITE 164 164 BY SIMILARITY.
FT MOD_RES 196 196 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT (BY SIMILARITY).
FT MOD_RES 198 198 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT (BY SIMILARITY).
SQ SEQUENCE 371 AA; 42741 MW; 4D97C41AC203C272 CRC64;
Query Match 65.0%; Score 1292; DB 1; Length 371;
Best Local Similarity 62.8%; Pred. No. 2.5e-77;
Matches 225; Conservative 70; Mismatches 63; Indels 0; Gaps 0;
OY 15 DEFPVLTHGGOYVDFGNFFETTKRPPIMPGRAVYGVSVLTLEMLNVAVKI 74
DB 10 EIKIPIHGEKYEYVNVGNFEVTSKIPPIQPGRGAYGCCATSEKKEEVAIKKI 69
OY 75 ANADIYADKRTREILRLHLDHENYIGLDVYPLPRESPDYATATLMDLDOI 134
DB 70 GNAEPENRDKARTREIKLLSHMDHENIKIKDIYRPDPREFENDVYIVYELMDIDLDOI 129
OY 135 IRSNOGLSEDHCOYFMQLGLGLAYIHSANVLRDLKPSNLLVNAICDLKICDEGLARP 194

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DB 130 IRSSQALTDHGOYFLYOLLGLKAYVHSANVLRDLKPSNLLVNAICDLKICDEGLART 189
OY 195 IENENMTEYVTRWYRAPELLNSDYTAIDWVSGCIEMELNKRPLFGKDHVOIR 254
DB 190 SEADFMTEYVTRWYRAPELLNCTEYTAIDWVSGCIELMKREPLFGRDVAQOLG 249
OY 255 LITELGTPTRADGFLONDEAKRYIRQLPQROQLAEVPHVPLAIDLVDKMLTFDP 314
DB 250 LITALLSPESDSDGLFLSDNARKYVKAHLPRVPRFSPQKFPDVSPLADLAERMLVFP 309
OY 315 TRRTVEBALDHPYLAUKLDAGDEPFCVPSFDFEQOIGEEQIKDMYQFEALSLNP 372
DB 310 AKRTIVEDALNHPFLISLHETNEBPVCSDFNEDEQASLSDDIKELINMNAIKFDP 367
RESULT 9
MPK5_ARATH STANDARD: PRT: 376 AA.
ID MPK5_ARATH
AC Q39025; O9SUS8;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mitogen-activated protein kinase homolog 5 (EC 2.7.1.-) (MAP kinase 5)
DE (AtMPK5).
GN MPK5 OR AT4G11330 OR FBL21.120.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustersoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCB1_TaxID=3702;
RN NCB1
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=94109583; PubMed=8282107;
RA Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,
RA Shinozaki K.;
RT "ATMPK5: a gene family of plant MAP kinases in Arabidopsis thaliana."
RL FEBS Lett. 336:440-444(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermair B., Mache R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohensei J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Gymnopoulos B., Chung Y.-J., Vandenbussche F.,
RA Brieken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weltzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Stevenen M., Dikse M.,
RA Moolman P., Klein Lanckhorst R., Rose M., Hauf J., Koetter P.,
RA Bernerster S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysschaert C., Giesen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail A., Bray-Allen K.,
RA Clark L., Doggett J., Hall S., Kay M., Leonard N., McIay K., Mayes R.,
RA Pettel A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Botkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fatmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argitlon A., Vitale D., Ligouri R., Piravandi E.,
RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chedof F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Hejnen L., Schwarz S., Scholler P., Heber S., Frances P., Bleke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,

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RA Parnell L., Dechia N., Guoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stenking T., Kalliock J., Graves T., Harmon G., Edwards J.,
RA Latrille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Manx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Splich J., Ryan E., Andrews S., Gelsel C., Layman D.,
RA Du H., All J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Gravat I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Chen E., Maria M., Matlessen R., Hancock W.R.,
RA Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana." ;
RL Nature 402:769-777(1999).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -1- CAUTION: Ref.2 sequences differ from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
DR EMBL: D21841; BAA04868.1; .
DR EMBL: AL096882; CAB51417.1; ALT_SEQ.
DR EMBL: AL16531; CAB81234.1; ALT_SEQ.
DR HSSP: P27703; IERK.
DR InterPro: IPR000719; Euk.pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR002527; MAP_kin.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PD00001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
DR Transferrase: Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Multigene family.
FT DOMAIN 43 329 PROTEIN KINASE.
FT NP_BIND 49 57 ATP (BY SIMILARITY).
FT BINDING 72 72 ATP (BY SIMILARITY).
FT ACT_SITE 169 169 BY SIMILARITY.
FT MOD_RES 201 201 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 203 203 (BY SIMILARITY).
FT MOD_RES 203 203 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 203 203 (BY SIMILARITY).
FT CONFLICT 59 59 A->P (IN REF. 1).
FT CONFLICT 276 277 AR->G (IN REF. 1).
SQ SEQUENCE 376 AA; 43207 MW; 2E8C0E5FC47685DF CRC64;
Query Match 64.6%; Score 1284; DB 1; Length 376;
Best Local Similarity 65.0%; Pred. No. 8.4e-77;
Matches 220; Conservative 62; Mismatches 62; Indels 0; Gaps 0;
QY 19 VLTNGQYVDFDIEGNEFFETTKYRPPIMPDIGAGYGVSVNTELENAVAKKINAF 78
DB 19 VLVHGGYFPGYVNYGNLFVSNKYVPIRIRIGAGYGVCAADSEHHEIAIKKIGAF 78
QY 79 DIYMAKRIKRLKRLHLDHENVIGIRVDYIPPLRRESVDYIATLMDTDJHQIIRSN 138
DB 79 IYVYDAKRIKRLKRLHLDHENVVYKIDIRPPKEDVYIVELMDTDJHQIIRSN 138
QY 139 OGISEDHCOYFMQOLRGKLYHSANVLHDKLPSNLLVANADKIKCDGCLARPNENE 198
DB 139 OGISEDHCOYFMQOLRGKLYHSANVLHDKLPSNLLVANADKIKCDGCLARPNENE 198

DB 139 QSLNDHCQYFQYQILNGKLYHSANVLHDKLPSNLLNSNCDKITDGLARTSETE 198
QY 199 NMTEYVYTRVYRAPPELLNSDSTYTAIDVWSVGCIFEMELNRRKPLFCGRDHYOIRLLE 258
DB 199 YMEYVYTRVYRAPPELLNSDSTYTAIDVWSVGCIFEMELNRRKPLFCGRDHYOIRLLE 258
QY 259 LIGTPTEADGFLONEDAKRYIRQLPQHPROOLAEPVHPVNPALADLVKMLTFDPTRTI 318
DB 259 LIGSPDASLEPLRSANARKYKELPKFPQNPNSARPPSNSTVADILEKMLVFDVPKRI 318
QY 319 TVEALDHPRLALHMDGDEPICVPSPDFEODGIGEDIKIMIVYALSLMP 372
DB 319 TVEALCYPLSLALHMDDEPVCNHSFHFEDPSSTEEBIKELWLESVKENP 372
RESULT 10
ID NTF3_TOBAC STANDARD; PRT; 372 AA.
AC Q40517;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitogen-activated protein kinase homolog NTF3 (EC 2.7.1.-) (P43).
GN NTF3.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Petit Havana SRI;
RX MEDLINE=9403334; PubMed=8219089;
RA Wilson C., Eller N., Gartner A., Vicente O., Heberle-Bors E.;
RT "Isolation and characterization of a tobacco cDNA clone encoding a
RT putative MAP kinase." ;
RL Plant Mol. Biol. 23:543-551(1993).
RN [2]
RP MOTAGENESIS.
RC STRAIN=cv. Petit Havana SRI;
RX MEDLINE=96061956; PubMed=7588752;
RA Wilson C., Anglmayer R., Vicente O., Heberle-Bors E.;
RT "Molecular cloning, functional expression in Escherichia coli, and
RT characterization of multiple mitogen-activated-protein kinases from
RT tobacco." ;
RL Eur. J. Biochem. 233:249-257(1995).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- DEVELOPMENTAL STAGE: DETECTED DURING GAMETOPHYTIC POLLEN
CC DEVELOPMENT AND CONSTITUTIVELY EXPRESSED IN EMBRYOGENIC POLLEN.
CC -1- PTM: VERY LOW AUTOPHOSPHORYLATION, ALTHOUGH DRAMATICALLY INCREASED
CC WHEN MN2+ IS ADDED TO THE REACTION INSTEAD OF MG2+.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X69971; CAA49592.1; .
DR HSSP: Q16539; IWRP.
DR InterPro: IPR000579; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PD00001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase: Serine/threonine-protein kinase; ATP-binding;
 KM Phosphorylation; Multigene family;
 FT DOMAIN 32 319 PROTEIN_KINASE;
 FT NP_BIND 38 46 ATP (BY SIMILARITY).
 FT BINDING 61 61 ATP (PROBABLE).
 FT ACT_SITE 158 158 BY SIMILARITY.
 FT MOD_RES 191 191 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT MOD_RES 193 193 (BY SIMILARITY).
 FT MOD_RES 193 193 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT MUTAGEN 61 61 K->R: INACTIVATION.
 FT SEQUENCE 372 AA; 42776 MW; 327735569F3EBA CAC64;
 SO
 Query Match 55.18; Score 1094.5; DB 1; Length 372;
 Best Local Similarity 58.18; Pred. No. 1,76-64;
 Matches 208; Conservative 63; Mismatches 82; Indels 5; Gaps 4;
 OY 19 VLTGGGVVDFGNGFETTKRPPIMPIGRGAYGVCVNLNEMVAVKKIANAF 78
 Db 11 IRTGGRKH--YSMOSLFEIDTKY-VPIKPIGRGAYGIVSSVNETEKVAIKINNAF 67
 OY 79 DIYDAKRLREIKLRHLDHENYIGLRDVIPLRREFSDVIATLMDTLHQIIRSN 138
 Db 68 ENRIDALRTLRKELRLRHLREHNYIALKDVMMPIHRSFKDYLYLVLEMDTLHQIIRSS 127
 OY 139 QGLSEDCQVRYMQLRLKATIHSAHYLRDLKSNLLVANCIDIKIDFGIARPN-EN 197
 Db 128 QTLSENDHQVYFLFQLRLKLYHSANILHRDLKPNGLINANCIDIKIDFGIARPSGKD 187
 OY 198 ENMEYVYTRYRRAPELLNSSDYTAIDVMSVGCIFEMELNRRKLPFGKQHVHRIILT 257
 Db 188 QFMREYVTRYRRAPELLNCDNIGTSDVMSVGCIFEMELNRRKLPFGKQHVHRIILT 247
 OY 258 ELIGTPTADLGLFQNDKAKRYIRQLPQHPROQLAEVPHVNPALIDLVMKLTFFDPTTR 317
 Db 248 NILTSQREDEIEFIDNPARKRYIKSLPYSPGTSRLPHAPHLAIDLQRLVLDPSKR 307
 OY 318 ITVEALDHPRLAKLHDAGDEIPCPVPSPFEOGIGEEQIKMTYDEALSINPEYA 375
 Db 308 ISVIEALQHPWSPLYDNPDPAPVPLINDIDED-IGETIREMWMSEILEYHPEAA 364

RESULT 11
 MPK1_ARATH STANDARD; PRT; 370 AA.
 ID MPK1_ARATH STANDARD; PRT; 370 AA.
 AC Q39021; Q9SY63;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitogen-activated protein kinase homolog 1 (EC 2.7.1.-) (MAP kinase 1)
 DE (AtMPK1).
 GN MPK1 OR AT1G10210 OR P14N23.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=9417172; PubMed=8130795;
 RA Mizoguchi T., Gotoh Y., Nishida E., Yamaguchi-Shinozaki K.,
 RA Hayashida N., Iwasaki T., Kamada H., Shinozaki K.;
 RT Characterization of two cDNAs that encode MAP kinase homologues in
 RT Arabidopsis thaliana and analysis of the possible role of auxin in
 RT activating such kinase activities in cultured cells.";
 RL Plant J. 5:111-122(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;

RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Atafifi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hutzar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maltli R., Marzilli A.,
 RA Maltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana";
 RL Nature 408:816-820(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SSP consortium (Salk/Stanford/PGSC).";
 RL submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
 CC PHOSPHORYLATION.
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN THE STEM. PRESENT IN THE
 CC LEAF, ROOT AND FLOWER, BUT NOT IN SEEDS.
 CC -1- INDUCTION: BY AUXIN (PROBABLE).
 CC -1- PTM: AUTOPHOSPHORYLATED ON THREONINE AND TYROSINE. AS WELL AS ON
 CC SERINE RESIDUES.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE SUBFAMILY.
 CC -----
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 DR EMBL; D14713; BA03535.1; -;
 DR EMBL; AC005489; AAD32871.1; -;
 DR EMBL; AY059937; AAL24419.1; -;
 DR HSSP; Q16539; IMFC.
 DR InterPro; IPR000719; MAP_kinase.
 DR InterPro; IPR003527; MAP_kin.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS01351; MAPK; FALSE_NEG.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase: Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation; Multigene family;
 FT DOMAIN 32 319 PROTEIN_KINASE;
 FT NP_BIND 38 46 ATP (BY SIMILARITY).
 FT BINDING 61 61 ATP (BY SIMILARITY).
 FT ACT_SITE 158 158 BY SIMILARITY.
 FT MOD_RES 191 191 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT MOD_RES 193 193 (BY SIMILARITY).
 FT MOD_RES 193 193 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT MUTAGEN 61 61 K->R: INACTIVATION.
 FT SEQUENCE 372 AA; 42776 MW; 327735569F3EBA CAC64;
 SO
 Query Match 55.18; Score 1094.5; DB 1; Length 372;
 Best Local Similarity 58.18; Pred. No. 1,76-64;
 Matches 208; Conservative 63; Mismatches 82; Indels 5; Gaps 4;
 OY 19 VLTGGGVVDFGNGFETTKRPPIMPIGRGAYGVCVNLNEMVAVKKIANAF 78
 Db 11 IRTGGRKH--YSMOSLFEIDTKY-VPIKPIGRGAYGIVSSVNETEKVAIKINNAF 67
 OY 79 DIYDAKRLREIKLRHLDHENYIGLRDVIPLRREFSDVIATLMDTLHQIIRSN 138
 Db 68 ENRIDALRTLRKELRLRHLREHNYIALKDVMMPIHRSFKDYLYLVLEMDTLHQIIRSS 127
 OY 139 QGLSEDCQVRYMQLRLKATIHSAHYLRDLKSNLLVANCIDIKIDFGIARPN-EN 197
 Db 128 QTLSENDHQVYFLFQLRLKLYHSANILHRDLKPNGLINANCIDIKIDFGIARPSGKD 187
 OY 198 ENMEYVYTRYRRAPELLNSSDYTAIDVMSVGCIFEMELNRRKLPFGKQHVHRIILT 257
 Db 188 QFMREYVTRYRRAPELLNCDNIGTSDVMSVGCIFEMELNRRKLPFGKQHVHRIILT 247
 OY 258 ELIGTPTADLGLFQNDKAKRYIRQLPQHPROQLAEVPHVNPALIDLVMKLTFFDPTTR 317
 Db 248 NILTSQREDEIEFIDNPARKRYIKSLPYSPGTSRLPHAPHLAIDLQRLVLDPSKR 307
 OY 318 ITVEALDHPRLAKLHDAGDEIPCPVPSPFEOGIGEEQIKMTYDEALSINPEYA 375
 Db 308 ISVIEALQHPWSPLYDNPDPAPVPLINDIDED-IGETIREMWMSEILEYHPEAA 364

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FT CONFLICT 310 310 V -> A (IN REF. 1).
FT CONFLICT 352 352 M -> I (IN REF. 1).
SQ SEQUENCE 370 AA: 42644 MW: F2962D7881C87A1B CRC64:
Query Match 54.3%; Score 1078; DB 1; Length 370;
Best Local Similarity 57.8%; Pred. No. 2e-63;
Matches 208; Conservative 59; Mismatches 89; Indels 4; Gaps 4;
OY 15 DFPVSLTHGQYQDFGFEFTTTRKPRPIMPICGAGYGVSVLTNENVAVKKI 74
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 6 DPNIGIRNEKH-YFSMQWQLFELDITKYM-PIDPISGAGVGVSSVNSTENKVAIKI 63
OY 75 ANAFDIYMDAKRTLRKILRLHLDHENVIGLRDVIPEPLRFESDYIATLMDTDLHQT 134
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 64 HNYENYIDILRLRLREKLRLHRLHENVIALKVMPIHMKSEKDYLYELMDTDLHQT 123
OY 135 IRSNOGSEDHQCYFMWQILRLGLKTIHSANVLRDLKPSNLVANANDLKICDGLARAS 183
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 124 IKSSQVLSNDHCQYFLQLRLGLKTIHSANVLRDLKPSNLVANANDLKICDGLARAS 183
OY 194 NINENNTETVYTRMYRAPPELLNNSDYTAIDVMSVGCIFMELMNRKPLFGKDHVQI 253
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 184 NTGQFETEVYTRMYRAPPELLNNSDYTAIDVMSVGCIFMELMNRKPLFGKDHVQI 253
OY 254 RLTELGLTPTLADGLFLOVEDAKRYTRQLPQHPROQLAEVFPVNPDLAIDVDMKLTED 313
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 244 KLIVNIIQSOREEDLEIFLDNPKAKRYTRSLPYSPGMSLISPGAHVLAIDLQKMLYFD 303
OY 314 PTPRTIVTEALDHPYLAKLDADGDEPICVPFSPFEOQIGEQIKDMVYQELSLNPE 373
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 304 PSKRISVSEALQHPYMAPLDPNANPPAQPVIDLVDDE-LREBIMREMMNEMLHYHPQ 362

RESULT 12
MAPK_PETHY STANDARD: PRT: 384 AA.
AC 040884;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitogen-activated protein kinase homolog 1 (EC 2.7.1.1-) (PMEK1).
GN MEK1.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ovule;
RX MEDLINE=95195161; PubMed=7888623;
RA Decrocoq-Ferrant V., Decrocoq S., van Went J., Schmidt E.,
RA Kreis M.;
RT "A homologue of the MAP/ERK family of protein kinase genes is
RT expressed in vegetative and in female reproductive organs of Petunia
RT hybrida."
RL Plant Mol. Biol. 27:339-350(1995).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN VEGETATIVE ORGANS SUCH AS LEAF,
CC ROOT, OR STEM. IN THE REPRODUCTIVE ORGANS, IT IS FOUND IN THE
CC OVARY, BUT NOT IN THE STAMEN.
CC -1- DEVELOPMENTAL STAGE: PRESENT DURING FLOWER DEVELOPMENT PRIOR TO
CC FERTILIZATION. AT EARLY STAGES OF OVULE DEVELOPMENT, THE
CC EXPRESSION IS UNIFORM THROUGHOUT THE OVULE. AT A LATER STAGE, IS
CC LOCALIZED ADJACENT TO THE EMBRYO SAC. WHEN THE FLOWER OPENS AND
CC POLLEN IS RELEASED, IT IS FOUND IN THE WHOLE OVULE AND IN THE
CC OUTER LAYER OF THE PLACENTA.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X83440; CAA58466.1; -.
DR HSP; P27703; IERK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS01017; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS01018; PROTEIN_KINASE_ST; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
KW DOMAIN 32 319 PROTEIN KINASE.
FT NE_BIND 38 46 ATP (BY SIMILARITY).
FT BINDING 61 61 ATP (BY SIMILARITY).
FT ACT_SITE 158 158 BY SIMILARITY.
FT MOD_RES 191 191 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 191 191 (BY SIMILARITY).
FT MOD_RES 193 193 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 193 193 (BY SIMILARITY).
SQ SEQUENCE 384 AA: 44444 MW: 7536CG960390EC58 CRC64:
Query Match 54.1%; Score 1075.5; DB 1; Length 384;
Best Local Similarity 57.0%; Pred. No. 3.1e-63;
Matches 204; Conservative 67; Mismatches 82; Indels 5; Gaps 4;
OY 19 VLRHGGYQDFDIFGNFEFTTTRKPRPIMPICGAGYGVSVLTNENVAVKIANAF 78
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 11 IRTPGKHY--YSMQSIFELDTKY-VPIKIGAGAGYGVSSVNRNENVAVKIANAF 67
OY 79 DIYMDAKRTLRKILRLHLDHENVIGLRDVIPEPLRFESDYIATLMDTDLHQTIRSN 138
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 68 ENRIDALRLRLREKLRLHRLHENVIALKVMPIQRSEKDYLYELMDTDLHQTIRSN 127
OY 139 QGSEDHQCYFMWQILRLGLKTIHSANVLRDLKPSNLVANANDLKICDGLARAPNI-EN 197
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 128 QTSLSNHCQYFLQLRLGLKTIHSANVLRDLKPSNLVANANDLKICDGLARATSSGKD 187
OY 198 ENNTEYVYTRMYRAPPELLNNSDYTAIDVMSVGCIFMELMNRKPLFGKDHVQIRLT 257
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 188 QPMTETVYTRMYRAPPELLNNSDYTAIDVMSVGCIFADVLGKRPVPGTECLNQLKTI 247
OY 258 ELTGPTLADGLFLOVEDAKRYTRQLPQHPROQLAEVFPVNPDLAIDVDMKLTPTTR 317
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 248 NIIQSOREEDLEIFLDNPKAKRYTRSLPYSPGMSLISPGAHVLAIDLQKMLYFDSKR 307
OY 318 ILYEALDHPYLAKLDADGDEPICVPFSPFEOQIGEQIKDMVYQELSLNPEYA 375
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 308 ISYWEALQHPYMAPLDPNANPPAQPVIDLVDDE-LVEETIREMWEELIHYHPFA 364

RESULT 13
MPK2_ARATH STANDARD: PRT: 376 AA.
AC 039022; Q9L058;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mitogen-activated protein kinase homolog 2 (EC 2.7.1.1-) (MAP kinase 2)
DE (AtMPK2).
GN MPK2 OR ATIG59580 OR T30E16.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```

OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=94177172; PubMed=8130795;
 RA Mitozuchi T., Gotoh Y., Nishida E., Yamaguchi-Shinozaki K.,
 RA Hayashida N., Iwasaki T., Kamada H., Shinozaki K.;
 RT "Characterization of two cDNAs that encode MAP kinase homologues in
 RT Arabidopsis thaliana and analysis of the possible role of auxin in
 RT activating such kinase activities in cultured cells.;
 RL Plant J. 5:111-122(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,
 RA Miltcher J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I.,
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vaysberg M., Vysotskai V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:816-820(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "RKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SFP consortium (Salk/Stanford/PGSC).";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
 CC PHOSPHORYLATION;
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN THE STEM. PRESENT IN THE
 CC LEAF, ROOT AND FLOWER, BUT NOT IN SEEDS.
 CC -1- INDUCTION: BY AUXIN (PROBABLE).
 CC -1- PTM: AUTOPHOSPHORYLATED ON THREONINE AND TYROSINE, AS WELL AS ON
 CC SPRINE RESIDUES.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: D14714; BAA03536.1; -;
 DR EMBL: AC009317; AAF7950.1; -;
 DR EMBL: AT035134; AAK59639.1; -;
 DR HSSP: Q16539; IWFC.
 DR InterPro: IPR000719; Euk_kinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase.1.
 DR ProDom: PD000001; Euk_pkinase.1.
 DR SMART: SM00220; S_TKc.1.
 DR PROSITE: PS001351; MAPK.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation; Multigene family.
 FT DOMAIN 32 319 PROTEIN KINASE.
 FT NP_BIND 38 46 ATP (BY SIMILARITY).
 FT BINDING 61 61 ATP (BY SIMILARITY).
 FT ACT_SITE 158 158 BY SIMILARITY.
 FT MOD_RES 191 191 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT MOD_RES 193 193 (BY SIMILARITY).
 FT MOD_RES 193 193 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT CONFLICT 33 33 (BY SIMILARITY).
 FT CONFLICT 299 299 V -> M (IN REF. 1).
 FT SEQUENCE 376 AA; 43124 MW; EDA07145A32CE25D CMC64;
 SQ
 Query Match 53.8%; Score 1069; DB 1; Length 376;
 Best Local Similarity 57.6%; Pred. No. 7.9e-63;
 Matches 209; Conservative 56; Mismatches 94; Indels 4; Gaps 4;
 OY 15 DEPSVLTGCGGVOPDIFGNFPEITTKYRPPIMPGRGAYGVCSVLTMLTENVAVYKRI 74
 DB 6 DEPNQIRNGKH-YESMGTLEFIDTKY-VPIKPIGRGAYGVCSVYRESNERVAIKKI 63
 OY 75 ANAFDIYMDAKRTLEIRILRLHENVIGLSDVIPPLRRESDVYATATLMDTLHQI 134
 DB 64 HVEFENRIDALETLEIKLRLRHENVYALKDVMANHRKFRKDYLYVELMDTLHQI 123
 OY 135 IRSNGLSDEHCOYTMQYLLGKIKIHSANVLRHRLKSNLLVYANCDLKICDEPLAR-P 193
 DB 124 IKSSQVLSNDHCQYFLFOLRLGKIKIHSANILRLKGNLLVYANCDLKICDEPLARTS 183
 OY 194 NIENNMTEYVYTRMYRRAPELLNSSDYTAIDVWVSCCIPMELNRRPLFGKDHVQI 253
 DB 184 NTKGFMTEYVYTRMYRRAPELLNCCDNGTSTIDWVSCCIPFELLGRKRPVPGTCLNOI 243
 OY 254 RLLELLGTPPEADIGFLQNEDEAKRYIRQLDPHQRLAEVFPVYPLAIDLVDKMLTFD 313
 DB 244 KLIIILSGREDEEDLEFDINPKAKRYIESLPSPGISRILPGANVALIDLLQGLVLD 303
 OY 314 PTRRTVEALDHPRLATLHDAGDEPICPVPSFDF-EQGGIGEGQIDMTIYQKLSNP 372
 DB 304 PSKRSTVEALQHPYMAPLDPSANPAOPVLDVDEDEDGAEIMELKMKEMIHYP 363
 OY 373 EYA 375
 DB 364 EAA 366
 RESULT 14
 MPK7_ARATH STANDARD; PRT; 368 AA.
 AC Q39027; O9S114;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitogen-activated protein kinase homolog 7 (EC 2.7.1.-) (MAP kinase 7)
 DE (AtMPK7).
 GN MPK7 OR AT2G18170 OR F8D23.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 NC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=94109583; PubMed=8282107;
 RA Mitozuchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,
 RA Shinozaki K.;
 RT "ATMPKs: a gene family of plant MAP kinases in Arabidopsis thaliana";
 RL FEBS Lett. 336:440-444(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;

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RX MEDLINE-20083467; PubMed-10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Kechum K.A., Lee J.J., Rooning C.M., Koo H.L.,
RA Moffit K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umeyan L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RT Nature 402:761-768(1999).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
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CC -----
DR EMBL: D21843; BAA04870.1; -.
DR EMBL: AC007212; AAD31349.1; -.
DR HSSP: Q16539; IMFC.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ARP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR TRANSFERASE: Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Multigene family.
FT DOMAIN 32 319
FT NP_BIND 38 46
FT BINDING 61 61
FT ACT_SITE 158 158
FT MOD_RES 191 191
FT MOD_RES 193 193
FT CONFLICT 104 104
FT CONFLICT 303 303
FT CONFLICT 324 324
FT CONFLICT 327 327
FT CONFLICT 366 366
SQ SEQUENCE 368 AA; 42299 MW; 64587EAC40C1A18 CRC64;

Query Match 53.4%; Score 1061; DB 1; Length 368;
Best Local Similarity 56.7%; Pred. No. 2,6e-62;
Matches 203; Conservative 63; Mismatches 88; Indels 4; Gaps 4;

17 PSYLTGAGGVQDFDGFNFETTKRPPIMPGRGAYGVGVLTGVLNTELEMAVAKKIAN 76
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db PNRKQGGKH-YYSMOTLEFIDTKY-VPIKPIGRGAYGVGVSSINRETERVAIKKIH 65
77 APDIYDAKRTLEIKLRLLDHEENVYGLRDVIPPPLRRESDVYIATLEMDTDLHQIIR 136
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db VFNRYDALRTLEIKLRVRHENVYALKDVALPANRSFKYVLYVELMDTDLHQIIR 125
66 VFNRYDALRTLEIKLRVRHENVYALKDVALPANRSFKYVLYVELMDTDLHQIIR 125
QY 137 SNGGLSEDCQIFMYQLGLKATYHSANVLHRLKDSNLVYANCDIKICDFGLARPNE 196
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 SSGSLSDDHCKYFLFOLLRLKYLKHSANILHRLKPGNLVYANCDIKICDFGLARTSG 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 197 NEN-MREYVYTRRYRAPPELLLNSSDYTAADVAVSGCIFELMNRKRPFGKGRHVHRI 255
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 186 NEQFMTEYVYTRMYRAPPELLLNSSDYTAADVAVSGCIFELMNRKRPFGKGRHVHRI 245
QY 256 LTELGTPTADLGFLEONEDAKRYIRLPOLPOHROOLEAFVPHVPLAIDLVDKMLTFDPPT 315
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 246 IINVGSGQESDIFDINPPARRIKSLPYSRGHLSNLYPQANPLAIDLORLALVDPT 305
QY 316 RRTVEBALDHPYLAKIHADGDEPICVPSFDEQOGEQIKMDIYQALSLNDE 373
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 KRISVTDALHPYWGAGLFDPGSNPPAHVPSLID-ENMEEPYIREMMNMMLYYHDE 362

RESULT 15
ERK1_DICDI
ID ERK1_DICDI STANDARD; PRT; 415 AA.
AC P42525;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Extracellular signal-regulated kinase 1 (EC 2.7.1.-) (ERK1) (MAP
DE kinase 1).
GN ERKA OR ERK1.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RX MEDLINE-95021228; PubMed-7935416;
RA Gaskins C.J., Maeda M., Firtel R.A.;
RT Identification and functional analysis of a developmentally
RT regulated extracellular signal-regulated kinase gene in Dictyostelium
RT discoideum."
RL Mol. Cell. Biol. 14:6996-7012(1994).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U11077; AAA59387.1; -.
DR HSSP: P27703; 1ERK.
DR DictyDb: DD01068; erkA.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ARP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Mitosis; Cell cycle; Phosphorylation.
FT DOMAIN 31 321
FT NP_BIND 37 45
FT BINDING 60 60
FT ACT_SITE 157 157
FT MOD_RES 191 191
FT MOD_RES 193 193
SQ SEQUENCE 415 AA; 47984 MW; C4912111260657B8 CRC64;

Query Match 52.3%; Score 1038.5; DB 1; Length 415;
Best Local Similarity 55.5%; Pred. No. 1,8e-61;

```


	Matches	196,	Conservative	61,	Mismatches	87,	Indels	9,	Gaps	4
OY	27	VQFDIFGNEFEETITKYRPIMPIDRGANGVIGSVLTNELNEMAVAKKIAMAEDIYDAKR	86	:	: : :	: : :	:	:	:	:
Dd	16	ISFYGGSOFTVPRRRY-SIVKCIHGAGVGWVSACKDNLTGEKVAIKIKIAKDNDLKTRC	74	:	:	:	:	:	:	:
OY	87	TURETKILRHLDHEWVIGADVIIPPLRREFSDVIYATLMTDLOHIIIRSNQGLSEBDC	146	:	:	:	:	:	:	:
Dd	75	TUREIHLRLRHEHEMELISKIDILKPSSKOPEDDVIYVELSMTDLOHIITSQPDLSDHC	134	:	:	:	:	:	:	:
OY	147	QYFMVLQLGLGYIHISANVYLHRDLKPSNLTVANACDLKCDGFAPRNINEN- ---MH-	202	:	:	:	:	:	:	:
Dd	135	QYFVYQMLRGKLKHHSANVYLHRDLKPSNLTIEDCLIKICDGLAR--VEDATHOGCFME	192	:	:	:	:	:	:	:
OY	203	YVVTBWYRAPELLNSSDYTAALDVWSVCIFPMEIMLNRRKPLFGCGKHVHQRIILLTELCT	262	:	:	:	:	:	:	:
Dd	193	YVATRWYRAPEVILTSMNKYTKAIDIMSWSCIPAEILLGRPLRGOKNYIQHTLIIFTTGS	252	:	:	:	:	:	:	:
OY	263	PTEALDGLFLONDAKARYIROL--POHPROQLAEVRPHVNPPLAIDLVDKKULTDPDRRTTY	320	:	:	:	:	:	:	:
Dd	253	PSEEDICNIJANOQAQOIFRSLSNMGNQOPKVNFAMPEPKAPMDAIDLERMIAYDPDSKRTLY	312	:	:	:	:	:	:	:
OY	321	EEALDHPLYLAKHDAGDEPICVPSPFSDEQGQSIGEEOIKDMATQEASLANEE	373	:	:	:	:	:	:	:
Dd	313	EEALAHPLVFQSILHDSDEPICLHKSTSLNEANDLNBDLLKELYNNMLAYHBE	365	:	:	:	:	:	:	:

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OM protein - protein search, using sw model

Run on: May 20, 2003, 00:00:32 : Search time 60 Seconds
(without alignments)
1287.794 Million cell updates/sec

Title: US-09-623-034-2
Perfect score: 1987
Sequence: 1 MADANMAGGQGFDPFSLV.....EQIKDMYQALSLNPEYA 375

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_todent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1987	100.0	375	10	040598
2	1958	98.5	375	10	08W406
3	1861	93.7	375	10	09LK22
4	1650	83.0	371	10	004694
5	1641	82.6	371	10	09M6S1
6	1635	82.3	365	10	09XG8
7	1634	82.2	371	10	024077
8	1490	75.0	369	10	09AXF2
9	1487	74.8	369	10	09FOM3
10	1483.5	74.7	394	10	09LK21
11	1482	74.6	393	10	004362
12	1473	74.1	369	10	043379
13	1472.5	74.1	399	10	09ZM75
14	1472	74.1	369	10	09FSE6
15	1471.5	74.1	389	10	09M534
16	1468	73.9	369	10	081599

17	1445	72.7	406	10	09ZM76	09ZM76 zea mays (m
18	1301	65.5	371	10	09AYN8	09AYN8 nicotiana t
19	1286	64.7	374	10	09ZP91	09ZP91 medicago sa
20	1285	64.7	363	10	09LK09	09LK09 arabidopsis
21	1279.5	64.4	393	10	09M175	09M175 arabidopsis
22	1258.5	63.3	369	10	09LMM5	09LMM5 arabidopsis
23	1232.5	62.0	389	10	09FX77	09FX77 chlamydomon
24	1219	61.3	406	10	08Z361	08Z361 arabidopsis
25	1112	56.0	370	10	09M545	09M545 oryza sativ
26	1087	54.7	372	10	09M6R8	09M6R8 oryza sativ
27	1085	54.6	369	10	09FOM2	09FOM2 oryza sativ
28	1076	54.2	369	10	09SMA9	09SMA9 oryza sativ
29	1034.5	52.1	368	10	09XFP5	09XFP5 prunus arne
30	1002	50.4	361	10	023236	023236 arabidopsis
31	957	48.2	265	10	08S376	08S376 oryza sativ
32	931	46.9	354	3	09OQ75	09OQ75 usciliago ma
33	927	46.7	351	3	04Z781	04Z781 pneumocysti
34	924	46.5	356	3	09Z246	09Z246 magnaporthe
35	921	46.4	352	3	09C1E0	09C1E0 neurospora
36	921	46.4	355	3	09C1I9	09C1I9 blumeria gr
37	920	46.3	355	3	09HGU2	09HGU2 fusarium ox
38	918	46.2	355	3	09C4B0	09C4B0 colletotric
39	918	46.2	355	3	09W0V9	09W0V9 glomerella
40	916	46.1	355	3	000859	000859 fusarium so
41	914	46.0	352	3	096X31	096X31 pyrenophora
42	914	46.0	355	3	09HG08	09HG08 botrytis ci
43	914	46.0	355	3	08X1A2	08X1A2 gibberella
44	907	45.6	355	3	09C137	09C137 gibberella
45	906	45.6	352	3	09UVN7	09UVN7 cochliobolus

ALIGNMENTS

RESULT 1
ID Q40598 PRELIMINARY; PRT; 375 AA.
AC Q40598;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE WIPK.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96123271; PubMed=8533090;
RA Seo S., Okamoto M., Sato H., Ishizuka K., Sano H., Ohashi Y.
RT "Tobacco MAP kinase: a possible mediator in wound signal transduction
RT pathways.";
RL Science 270:1988-1992(1995).
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: D61377; BAA09600.1; -;
DR HSP: Q16539; IWPK
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Euk_Pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferrase.
SO SEQUENCE 375 AA; 42853 MW; 23480EDBA1EACBD8 CRC64;
Query Match 100.0%; Score 1987; DB 10; Length 375;
Best Local Similarity 100.0%; Pred. No. 9.8e-162;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADANMGAGGQPPDFPSVLTGGOYVQDFIFGNFEITTKYRPPIMPGRGAGYICSV 60
 DB 1 MADANMGAGGQPPDFPSVLTGGOYVQDFIFGNFEITTKYRPPIMPGRGAGYICSV 60
 QY 61 LNTLEINEMVAVKITANAFDIYMDAKRTLREIKLRHLDHENVIGLRVYIPPLRERSDV 120
 DB 61 LNTLEINEMVAVKITANAFDIYMDAKRTLREIKLRHLDHENVIGLRVYIPPLRERSDV 120
 QY 121 YIATELMDTDLHQIIRSNQGLSEDCQYFMQYLLRGLKYHSANVLRHDLKPSMLLVAN 180
 DB 121 YIATELMDTDLHQIIRSNQGLSEDCQYFMQYLLRGLKYHSANVLRHDLKPSMLLVAN 180
 QY 181 CDLKICPGLARPIENENMTEYVTRMYRAPPELLNNSDYTAIDVWSVCIFMELMNR 240
 DB 181 CDLKICPGLARPIENENMTEYVTRMYRAPPELLNNSDYTAIDVWSVCIFMELMNR 240
 QY 241 KPLFGGDHWHQIRLTLELSTPTFADLGLQNEADAKRYIRQLPQHPROQLAEVFPHPNP 300
 DB 241 KPLFGGDHWHQIRLTLELSTPTFADLGLQNEADAKRYIRQLPQHPROQLAEVFPHPNP 300
 QY 301 LAIDLVDKMLTFDPTRRTVEALDHPYLAKLHDAGDEPICPVPSFDEQOGIGEQIK 360
 DB 301 LAIDLVDKMLTFDPTRRTVEALDHPYLAKLHDAGDEPICPVPSFDEQOGIGEQIK 360
 QY 361 DMITYOEALSLNPEYA 375
 DB 361 DMITYOEALSLNPEYA 375

RESULT 2

Q8M406 PRELIMINARY; PRT; 375 AA.
 ID O8M406;
 AC O8M406;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Wound induced protein kinase.
 GN WIPK.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sano H., Yap Y.K.;
 RT "Genome organisation of WIPK gene in tobacco."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB052964; BAB79636.1; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR ProDom: PD000001; Euk_pkinase.1.
 DR SMART: SM00220; S_TKc.1.
 DR SMART: SM00219; TYKc.1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
 KW kinase.
 SQ SEQUENCE 375 AA; 42898 MW; 9BA49C8C39E1C88F CRC64;

Query Match 98.5%; Score 1958; DB 10; Length 375;
 Best Local Similarity 98.4%; Pred. No. 3e-159;
 Matches 369; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MADANMGAGGQPPDFPSVLTGGOYVQDFIFGNFEITTKYRPPIMPGRGAGYICSV 60
 DB 1 MADANMGAGGQPPDFPSVLTGGOYVQDFIFGNFEITTKYRPPIMPGRGAGYICSV 60

QY 61 LNTLEINEMVAVKITANAFDIYMDAKRTLREIKLRHLDHENVIGLRVYIPPLRERSDV 120
 DB 61 LNTLEINEMVAVKITANAFDIYMDAKRTLREIKLRHLDHENVIGLRVYIPPLRERSDV 120
 QY 121 YIATELMDTDLHQIIRSNQGLSEDCQYFMQYLLRGLKYHSANVLRHDLKPSMLLVAN 180
 DB 121 YIATELMDTDLHQIIRSNQGLSEDCQYFMQYLLRGLKYHSANVLRHDLKPSMLLVAN 180
 QY 181 CDLKICPGLARPIENENMTEYVTRMYRAPPELLNNSDYTAIDVWSVCIFMELMNR 240
 DB 181 CDLKICPGLARPIENENMTEYVTRMYRAPPELLNNSDYTAIDVWSVCIFMELMNR 240
 QY 241 KPLFGGDHWHQIRLTLELSTPTFADLGLQNEADAKRYIRQLPQHPROQLAEVFPHPNP 300
 DB 241 KPLFGGDHWHQIRLTLELSTPTFADLGLQNEADAKRYIRQLPQHPROQLAEVFPHPNP 300
 QY 301 LAIDLVDKMLTFDPTRRTVEALDHPYLAKLHDAGDEPICPVPSFDEQOGIGEQIK 360
 DB 301 LAIDLVDKMLTFDPTRRTVEALDHPYLAKLHDAGDEPICPVPSFDEQOGIGEQIK 360
 QY 361 DMITYOEALSLNPEYA 375
 DB 361 DMITYOEALSLNPEYA 375

RESULT 3

Q9LKZ2 PRELIMINARY; PRT; 375 AA.
 ID Q9LKZ2;
 AC Q9LKZ2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE MAP kinase 1.
 GN MK1.
 OS Capsicum annuum (bell pepper).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
 OX NCBI_TaxID=4072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Back K., Han O., Shin H.-J., Kim K.-U.;
 RT "Molecular cloning and cultivar specific expression of MAP kinase from Capsicum annuum."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF247135; AAF81419.1; -
 DR HSSP: Q16539; IWFC.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR ProDom: PD000001; Euk_pkinase.1.
 DR SMART: SM00220; S_TKc.1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 375 AA; 42954 MW; AE78396ZACS240C4 CRC64;

Query Match 93.7%; Score 1861; DB 10; Length 375;
 Best Local Similarity 92.5%; Pred. No. 5.8e-151;
 Matches 347; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 MADANMGAGGQPPDFPSVLTGGOYVQDFIFGNFEITTKYRPPIMPGRGAGYICSV 60
 DB 1 MADANMGAGGQPPDFPSVLTGGOYVQDFIFGNFEITTKYRPPIMPGRGAGYICSV 60
 QY 61 LNTLEINEMVAVKITANAFDIYMDAKRTLREIKLRHLDHENVIGLRVYIPPLRERSDV 120
 DB 61 LNTLEINEMVAVKITANAFDIYMDAKRTLREIKLRHLDHENVIGLRVYIPPLRERSDV 120

Qy	121	YATIELMDTDHOIIRSNQGISSEBHCQYFMOLLRGKTYHSANVLRDLKPSNLVYMAN	180
Db	121	YATIELMDTDHOIIRSNQGISSEBHCQYFMOLLRGKTYHSANVLRDLKPSNLVYMAN	180
Qy	181	CDLKICDEGLARPNIENENMTEYVVTWYRAPPELLNSSDYTAIDWWSGCCIFMELMNR	240
Db	181	CDLKICDEGLARPNIENENMTEYVVTWYRAPPELLNSSDYTAIDWWSGCCIFMELMNR	240
Qy	241	KPLFGGKDWHQIRLLTELLGTPTEADLIGFLQONEDAKRYTROLRPOHRQOGLAEFFPHVP	300
Db	241	KPLFGGKDWHQIRLLTELLGTPTEADLIGFLQONEDAKRYTROLRPOHRQOGLAEFFPHVP	300
Qy	301	LAIDVDMKMLFEDPRTTATVEALDHDHYLAKLHHGAGEPICAPVPESDFEQQGIGGEBOIK	360
Db	301	LAIDVDMKMLFEDPRTTATVEALDHDHYLAKLHHGAGEPICAPVPESDFEQQGIGGEBOIK	360
Qy	361	DMIVQALSLNPEYA 375	
Db	361	DMIVQALSLNPEYA 375	

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RESULT 4
ID      004694      PRELIMINARY;      PRT.      371 AA.
AC      004694;
DT      01-JUL-1997 (TREMBLrel. 04, Created)
DT      01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT      01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE      MAP kinase I.
OS      Petroselinum crispum (Parsley) (Petroselinum hortense).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC      Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.
OX      NCBI_TaxID=4043;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97342856; PubMed=9197271;
RT      Listerink W., Kroj T., zur Nieden U., Hirt H., Scheel D.;
RT      "Receptor-mediated activation of a MAP kinase in pathogen defense of
RT      plants.";
RL      Science 276:2054-2057(1997).
CC      -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR      HEMBL; Y12785; CA73323.1; -.
DR      HSSP; I16539; IMPC.
DR      InterPro; IPR000719; Euk_pkinase.
DR      InterPro; IPR003527; MAP_kin.
DR      InterPro; IPR002290; Ser_thr_kinase.
DR      Pfam; PF00069; Pkinase; 1.
DR      ProDom; PD000001; Euk_pkinase; 1.
DR      SMART; SM00220; S_TKC; 1.
DR      PROSITE; PS01351; MAPK; UNKNOWN 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW      ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW      Sequence 371 AA; 42794 MW; 66DA68328221B3EB CRC64;

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Query Match	83.0%;	Score 1650;	DB 10;	Length 371;
Best Local Similarity	81.7%;	Pred. No. 6.4e-133;		
Matches 300;	Conservative 39;	Mismatches 28;	Indels 0;	Gaps 0;

Qy	9	GGGQPPPEPSVLTGGGQVODDFGNGFFETLTKXRPPIIMPJIGRAVCIYCSVYLTETLNNM	68
		Ll: : : : : : : : : : : : : : :	
Dd	5	GDGQYTPERPAQTGHGQGFQVNIENGLEFQYTKKTRPPIIMPJIGRAVCIYCSVYLTETLNNM	64
Qy	69	VAVKKIANAFPIYMDAKRTLREIKLRLHLDHENYIGLRDVIPPPRLRESDVIYATLMD	128
		Ll: : : : : : : : : : : : : : :	
Dd	65	VAVKKIANAFNYMDAKRTLREIKLRLHLDHENYIATTDVIPPRLREPFDDVIYATLMD	124
Qy	129	TDLHDIINSNGLSEDDHCQYFPMYOLLGRLKATHSANVLAJHDKRSNLLVANANDKICDF	188
		Ll: : : : : : : : : : : : : : :	
Dd	125	TDLHDIINSNGLSEDDHCQYFLYOLLGRLKATHSANVILHDKRSNLLVANANDKICDF	184

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OY 189 GLARPNIENEMTEYVUTRTYRAPELLNNSDYTAIDWMSVGCIFELMANKRPLFGKD 248
      ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
Db 185 GLARINTEDEPMTEYVUTRWYRAPELLNNSDYTAIDWMSVGCIFYMELNNRPLFGKD 244
      ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
OY 249 HVHOLRIITELLGPTFADGIFLONEDAKRTIOLPOHPROOLAEPYRHNPLAIDLVDK 308
      ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
Db 245 HVHOLRIITELLGPTFADGIFVFNEDAKRTIOLPRHPORLYOLRYOHNPLAIDLIDK 304
      ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
OY 309 MLTEPPTRRIRIVEBALDHPYLAKNDADEPFCIVPSPFDEOQIGTEEOIKIMITYOAL 368
      ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
Db 305 MLTEPSPKRIRIVEEALNHPYLAKNDADEPFCIKPSPSFEETANHGEEOIKIMITYOAL 364
      ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
OY 369 SLNPEYA 375
      : : : :
Db 365 AFNPDCA 371
      : : : :

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Q9M6S1	PRELIMINARY;	PRT;	371 AA.
ID	Q9M6S1		
AC	Q9M6S1;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	MAP kinase 3.		
GN	MAPK3.		
OS	Pisum sativum (Garden pea).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;		
OC	Eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.		
OX	NCBI_TaxID=3888;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV, ALASKA; TISSUE=OVARY;		
RX	MEDLINE=21003323; PubMed=11117261;		
RA	Marcoite M.J., Cardonell J.;		
RT	"Transient expression of a pea MAP kinase gene induced by gibberellin		
RT	acid and 6-benzyladenine in unilluminated pea ovaries.";		
RL	Plant Mol. Biol. 44:177-186(2000).		
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
DR	EMBL; AF153061; AAF73236.1; -;		
DR	HSSP; Q16539; IMFC.		
DR	InterPro; IPR000719; Euk_pkinase.		
DR	InterPro; IPR003527; MAP kin.		
DR	InterPro; IPR002290; Ser_thr_pkinase.		
DR	Pfam; PF00069; pkinase.1.		
DR	ProDom; PD000001; Euk_pkinase.1.		
DR	SMART; SM00220; S_TKc.1.		
DR	PROSITE; PS01351; MAPK; UNKNOWN.1.		
DR	PROSITE; PS00107; PROTEIN KINASE_AFP; 1.		
DR	PROSITE; PS00011; PROTEIN KINASE_DOM; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		
DR	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.		
SC	SEQUENCE 371 AA; 42919 MW; A6F42D295CF48BC CRC64;		

Query Match	82.6%;	Score 1641;	DB 10;	Length 371;
Best Local Similarity	83.1%;	Pred. No. 3.8e-132;		
Matches 300; Conservative	37;	Mismatches 24;	Indels 0;	Gaps 0

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0Y      15 DEPSVLTHGGGYOVDFDINGNEETLTKYRPIIMPJGGAAGYVSVYLTNETNEVAAKI  74
Db      11 EPPAVOHTGGGFVQVQYNVGNLFVEYTKARPPIMPJGGAAGYVSVSLTNETNELVAAKI  70
0Y      75 ANAEDIYMDARPTLREIKLRLHDHENYIGLDVYIPPLRRESVDYIATELMDTDLHQI  134
Db      71 ANAEFNHMDARKTREIKLRLHDHENYIGLDVYIPPLRREFNDVYITTELMDDTLHQI  130
0Y      135 IRSNGQSEEDHCQYFPMVOLLGKLYTHISANVLHBDLKPNSLIVANCDLTCOFGGLARPN  194
Db      131 IRSNQNLSDEHCQYFVLQILGLKRTYHSANLIRHDLKPSNLLIVANCDLTIIDGLARPT  190
0Y      195 IENENMEYEVYTRWRAPPELLNLSDDVYALDVWSVCCIMPELNNRPPLEGGGDHWHQIR  254

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Db 191 MENDEMEYVYTRMYRAPELLNSDYTSADVWSVGCIFMELNKKKPLFGKDHVQMR 250
QY 255 LTTELLGPTPEADGFLONEDAKRYIRQLPQHPROQLAEVPHVPLAIDLVDKMLTFDP 314
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 251 LTTELLGPTPDADGLVANDAKRYIRQLPQHPROQLAEVPHVPLAIDLVDKMLTFDP 310
QY 315 TRRTIVEBALDHPYLAUKLDAGDEPICVPSFDFEEOGIGEEQIKDMITOEALSLNDEY 374
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 311 TRRTIVEBALDHPYLAUKLDAGDEPICVPSFDFEEOGIGEEQIKDMITOEALSLNDEY 370
QY 375 A 375
    :|||:
Db 371 A 371

RESULT 6
QY 09XG18 PRELIMINARY: PRT: 365 AA.
AC 09XG18;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE MAP kinase.
OS Ipomoea batatas (Sweet potato) (Batale).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids I; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=4120;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, TAINONG 57; TISSUE=LEAF;
RA TO K.Y., Suen D.F., Chen S.C.G.;
RT "Cloning Of A Sweet Potato Leaf cDNA (Accession No. AF149424) Encoding
RT Mitogen-Activated Protein Kinase. (PGR99-135).";
RL Plant Physiol. 121:312-312(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF149424; AAD37790.1; -.
DR HSSP: P27703; IERK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR ProDom: PD000001; Euk_pkinase.1.
DR SMART: SM00220; S_TKc.1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM.1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 365 AA; 41745 MW; 4A2998BA61178427 CRC64;

Query Match 82.3%; Score 1635; DB 10; Length 365;
Best Local Similarity 82.8%; Pred. No. 1.2e-131;
Matches 304; Conservative 35; Mismatches 24; Indels 4; Gaps 2;

QY 9 GGGGPPDPSPVLTGGOYVQDFIGNFEITTKYRPPIMPGRGAYGIVCSVLTNEM 68
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 GGG--DELAOTGGOYVQDFIGNFEITTKYRPPIMPGRGAYGIVCSVLTNEM 59
QY 69 VAAVKIAPFIYMDAKRTREIKLRHLDHENYIGLDVYIPPLRREFSDVYATETLMD 128
    ||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 VAIKKIADAFNYMDAKRTREIKLRHLDHENYIAIDVYIPPLRREFSDVYATETLMD 119
QY 129 TDLHQIIRNSNGLSDEHCQYFMYQLRLGKIYHSANVLRHDLKPSNLLVANCCLKICDF 188
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 TDLHQIIRNSNGLSDEHCQYFMYQLRLGKIYHSANVLRHDLKPSNLLVANCCLKICDF 179
QY 189 GLARPNIENEMTEYVYTRMYRAPELLNSDYTAIDVWSVGCIFMELNKKKPLFGSKD 248
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 GLARTNIENEMTEYVYTRMYRAPELLNSDYTAIDVWSVGCIFMELNKKKPLFGCKD 239
QY 249 HVHQRILTELLGPTPEADGFLONEDAKRYIRQLPQHPROQLAEVPHVPLAIDLVDK 308
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 240 HVHQRILTELLGPTPEADGFLONEDAKRYIRQLPQHPROQLAEVPHVPLAIDLVDK 299
QY 309 MLTFDPTRTIVEBALDHPYLAUKLDAGDEPICVPSFDFEEOGIGEEQIKDMITOEAL 368
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 MLTFDPTRTIVEBALDHPYLAUKLDAGDEPICVPSFDFEEOGIGEEQIKDMITOEAL 358
QY 369 SLNDEYA 375
    :|||:
Db 359 AMNPGYA 365

RESULT 7
QY 024077 PRELIMINARY: PRT: 371 AA.
AC 024077;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Protein kinase.
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eusterids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
OX NCBI_TaxID=3879;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97008170; PubMed=885346;
RA Jonak C., Kiegl S., Ligerer S., Ligerer W., Barker P., Huskisson N., Hirt H.;
RT "signaling in plants: a mitogen-activated protein kinase pathway is
RT activated by cold and drought.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:11274-11279(1996).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: X82270; CA57721.1; -.
DR HSSP: Q16539; IMFC.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR ProDom: PD000001; Euk_pkinase.1.
DR SMART: SM00220; S_TKc.1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM.1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 371 AA; 42963 MW; 8CC390454E4350E CRC64;

Query Match 82.2%; Score 1634; DB 10; Length 371;
Best Local Similarity 82.8%; Pred. No. 1.5e-131;
Matches 299; Conservative 38; Mismatches 24; Indels 0; Gaps 0;

QY 15 DFPSTLTHGGOYVQDFIGNFEITTKYRPPIMPGRGAYGIVCSVLTNEMVAVVKI 74
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 11 EFPVOTGGOYVQYVNGVGNLFVYAKRPPIMPGRGAYGIVCSVLTNEMVAVVKI 70
QY 75 ANAEDIYMDAKRTREIKLRHLDHENYIGLDVYIPPLRREFSDVYATETLMDTDLHQI 134
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 71 ANAEDNMDAKRTREIKLRHLDHENYIGLDVYIPPLRREFSDVYATETLMDTDLHQI 130
QY 135 IRSNGLSDEHCQYFMYQLRLGKIYHSANVLRHDLKPSNLLVANCCLKICDGLARP 194
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 131 IRSNGLSDEHCQYFMYQLRLGKIYHSANVLRHDLKPSNLLVANCCLKICDGLARP 190
QY 195 IENEMTEYVYTRMYRAPELLNSDYTAIDVWSVGCIFMELNKKKPLFGSKDHVQIR 254
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 191 MESDPMTYVYTRMYRAPELLNSDYTSADVWSVGCIFMELNKKKPLFGSKDHVQMR 250
QY 255 LTTELLGPTPEADGFLONEDAKRYIRQLPQHPROQLAEVPHVPLAIDLVDKMLTFDP 314
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 251 LTTELLGPTPDADGLVANDAKRYIRQLPQHPROQLAEVPHVPLAIDLVDKMLTFDP 310
QY 315 TRRTIVEBALDHPYLAUKLDAGDEPICVPSFDFEEOGIGEEQIKDMITOEALSLNDEY 374

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Db      311  TRRTVEBALAHPLYLEKLDHVADPEICMEPPSEFEQOHLDERQIKEMITREALAINPEX 370
Oy      375  A 375
Db      371  A 371

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RESULT 8
Q9AXF2
ID Q9AXF2 PRELIMINARY; PRT; 369 AA.

DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE MAP_Kinase BIK1.
OS Oryza sativa (rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzeae; Oryza.
OX NCBI_Taxid:4530.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. YUANFENGZAO;
RA Song F., Goodman R.M.;
RT "OSBIK1, a novel MAP kinase from rice that is involved in systemic
RT acquired resistance";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF352873; AAK01710.1; -.
DR HSSP: Q16539; 1WFC.
DR InterPro: IPR000719; MAP_kinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR001290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TYKc; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 369 AA: 43029 MW: 417D88EB32635F2D3 CRC64:

Query Match	75.0%	Score 1490;	DB 10;	Length 369;
Best Local Similarity	72.3%	Pred. No. 3.1e+19;		
Matches 264; Conservative	59;	Mismatches 42;	Indels 0;	Gaps 0;

QY	10	GGGPPDPSPVYTHGGGVYOFIFCNFPFITIKYPPPIPIPIGRGAYGVCSTUNLEUMY	69
Dd	3	GAPAAEFRRPMTTHGGGRILYDIFCNKPEVTYKPKPPIMPPIGRGAYGVCSTUNLEUMY	62
QY	70	AVKIAANAFDIYMDAKRTLRKIKLLRHLDHENVYIGLRDVPPLPIRREDSVYIATELMDT	123
Dd	63	AIKKIAANAFFNMDAKRTLRKIKLLRHLDHENVYIGLRDVPPLPIPOAFNDVYIATELMDT	122
QY	130	DLHGIIIRSNQGLSDHCQYFMYGOLLRGKITYHSANVYLRDLKPSNLLVYNAACDLKIDFG	189
Dd	123	DLHHIIRSNQGLSEHCOYFLYQTLRLGKITYHSANVYLRDLKPSNLLVYNAACDLKIDFG	188
QY	190	LARPNIENKMTVEYVTRWYRAPPELLNSSDYTAIDVWSVGCIFMELMNKRPLEGGKH	245
Dd	183	LARSSSSDMATVEYVTRWYRAPPELLNSTDYSAIDVWSVGCIFMELINROPLEPGKH	244
QY	250	VHQIRLLLETLGTPEADIGFLOEDMDKARYIROLPOHROOLAEEVFPVYNLAIDLVDKM	309
Dd	243	MHQIRLLTEVIGTPTDDELGIIRREDKARKYRHLPOYPRKRFASMFPRVYOPALDLIERM	308
QY	310	LTDPPTRRIIVEALDHPYRLAKLHDADGDEPICVPVSPFDEQOIGEGQIKDMITYOALS	366
Dd	303	LTFNPRLORITVEALDHPYERLHDIDDEPICLPSPFDEFOKRLNDEMQOLTFENAI	365

RESULT 9
Q9FQM3
ID Q9FQM3 PRELIMINARY; PRT; 369 AA

DT 01-MAR-2001 (TREMBlrel.. 16, Created)
 DT 01-MAR-2001 (TREMBlrel.. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel.. 21, Last annotation update)
 DE MAP kinase 1 (MAP kinase MAPK5a).
 GN MAPK5.
 OS *Oryza sativa* (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; *Oryza*.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wen J.-Q., Imai R.,
 RT "A MAP kinase cascade component, OSMAP1 was induced by chilling stress
 in rice." (DEC-1999) to the EMBL/Genbank/DBJ databases.
 RL Submitted

DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 369 AA; 42995 MW; 417D81732635F2D3 CRC64;

[illegible]

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QY 310 LTFDPRTIYVEALDHPYLAKLHDAGDEPTCPVPFSFDEQOIGEOIKDMITOEALIS 369
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 303 LTFNPLQRIYVEALDHPYLAKLHDAGDEPTCPVPFSFDEQOIGEOIKDMITOEALIS 362
QY 370 LNP 372
      |||
Db 363 MNP 365

RESULT 10
09Lkz1
ID 09Lkz1 PRELIMINARY: PRT: 394 AA.
AC 09Lkz1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE MAP kinase 2.
GN MK2.
OS Capsicum annuum (Bell pepper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
RN [1]
RP SEQUENCE FROM N.A.
RA Back K., Han O., Shin H.-U., Kim K.-U.;
RT "Molecular cloning and cultivar specific expression of MAP kinase from
RT Capsicum annuum."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF247136; AAF81420.1; -.
DR HSSP: P27703; IERK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 394 AA; 45196 MW; 788FF8C76D383C15 CRC64;

Query Match 74.7% Score 1483.5; DB 10; Length 394;
Best Local Similarity 75.0%; Pred. No. 1.2e-118;
Matches 270; Conservative 43; Mismatches 46; Indels 1; Gaps 1;

QY 15 DEPSVLTHTGGGVQEDTGNFETTKRPPIMPGRCAYIGSVLTLELNMVAVAKI 74
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 33 NIPATLSGGRTIYNIFGNVEYAKYKPPIMPGRCAYIGSVLTLELNMVAVAKI 92
QY 75 ANADIVYADARTLEIKLRLHLDHENYIGLRDVPPLRREFSQVYATATLMDTDLQI 134
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 93 ANADINKIDAKRTLEIKLRLHLDHENYIGLRDVPPLRREFSQVYATATLMDTDLQI 152
QY 135 IRSNOGLSEHCQYFMTQLRGLKTIHSANVLAHRDLKPSNLLVLANCDLKTCDGLAPN 194
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 153 IRSNOGLSEHCQYFMTQLRGLKTIHSANVLAHRDLKPSNLLVLANCDLKTCDGLAVT 212
QY 195 IENENMTEYVYTRWRAPPELLNNSDYTAALDVMSVGCIFEMLNKRKLFGSKDHVHQR 254
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 213 SETFMTEYVYTRWRAPPELLNNSDYTAALDVMSVGCIFEMLNKRKLFGSKDHVHQR 272
QY 255 LTFELGPTTADIGFLONEDAKRYIRLPQHPROQLAEVPHVPLAIDLVDKMLTFDP 314
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 273 LLMELIGTPSAEMEFLLNENAKRYIRLPQHPROQLAEVPHVPLAIDLVDKMLTFDP 331
QY 315 TRITVEALDHPYLAKLHDAGDEPTCPVPFSFDEQOIGEOIKDMITOEALISLNP 374
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 332 RRRLVEALDHPYLAKLHDAGDEPTCPVPFSFDEQOIGEOIKDMITOEALISLNP 391
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RESULT 11
004362
ID 004362 PRELIMINARY: PRT: 393 AA.
AC 004362;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Salicylic acid-activated MAP kinase.
GN NTSIPK.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=XANTHI NC.
RC Zhang S., Kleissig D.F.;
RT "Salicylic acid activates a 48-kilodalton MAP kinase in tobacco."
RL Plant Cell 9:0-0(1997).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U94192; AAB58396.1; -.
DR HSSP: P27703; IERK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 393 AA; 45162 MW; 4C707023F1E0904C CRC64;

Query Match 74.6% Score 1482; DB 10; Length 393;
Best Local Similarity 71.5%; Pred. No. 1.6e-118;
Matches 274; Conservative 46; Mismatches 51; Indels 12; Gaps 2;

QY 3 DANWAGSGGPP-----DEPSVLTHTGGGVQEDTGNFETTKRPPIMPGR 51
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 9 DTMSDACAEGPPAPQPVYAGMDNIPATLSHGGRITQYNIFGNVEYAKYKPPILPIGK 68
QY 52 GAYGIVCSVLTLELNMVAVKRIANAFDIYDAKRTLEIKLRLHLDHENYIGLRDVP 111
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 69 GAYGIVCSVLTLELNMVAVKRIANAFDIYDAKRTLEIKLRLHLDHENYIGLRDVP 128
QY 112 PLRREFSQVYATATLMDTDLQIIRSNOGLSEHCQYFMTQLRGLKTIHSANVLAHRDLK 171
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 129 POREAFNPNVYATATLMDTDLQIIRSNOGLSEHCQYFMTQLRGLKTIHSANVLAHRDLK 188
QY 172 PSNLLVLANCDLKTCDGLAPNTENMTEYVYTRWRAPPELLNNSDYTAALDVMSV 231
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 189 PSNLLVLANCDLKTCDGLAPNTENMTEYVYTRWRAPPELLNNSDYTAALDVMSV 248
QY 232 CIFEMLNKRKLFGSKDHVHQRILRLTELGTPTADIGFLONEDAKRYIRLPQHPROQL 291
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 249 CIFEMLNKRKLFGSKDHVHQRILRLTELGTPTADIGFLONEDAKRYIRLPQHPROQL 307
QY 292 AEFVPHVPLAIDLVDKMLTFDPTRITVEALDHPYLAKLHDAGDEPTCPVPFSFDEQ 351
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 308 TEKPPHVPATIDLVKMLTFDPTRITVEALDHPYLAKLHDAGDEPTCPVPFSFDEQ 367
QY 352 OGIGEOIKDMITOEALISLNP 374
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 368 HALTEQMKELTYRSLAFNPEY 390

RESULT 12
043379
ID 043379 PRELIMINARY: PRT: 369 AA.
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AC Q43379;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, last annotation update)
DE MAP kinase.
GN ASMAP1.
OS Avena sativa (Oat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Avenae; Avena.
OX NCBI_TaxID=4498;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. RHANNON; TISSUE=ALEURONE;
RX MEDLINE=95284341; PubMed=7766874;
RA Huttly A.K., Phillips A.L.;
RT "glibetellin regulated expression in oat aleurone cells of two kinases
RT that hrow homology to nap kinase and a ribosomal protein kinase.";
RL Plant Mol. Biol. 27:1043-1052(1995).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: X79993; CAA56314.1; -.
DR HSSP: Q16539; IMFC.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Prodom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SO SEQUENCE 369 AA; 42871 MW; 2A76A50A867A63f CRC64;

Query Match 74.1%; Score 1473; DB 10; Length 369;
Best Local Similarity 72.9%; Pred. No. 8.8e-118;
Matches 266; Conservative 52; Mismatches 47; Indels 0; Gaps 0;
QY 10 GGQFPDFPSVLTHGGQYQVDFGCFNFETTKYRPPIMPICGAGYCVSLATELNEMV 69
DB 3 GAPAEEFPPTMGGRFLYNIFGQFITSKYQPPIMFIGAGYCVSNMFETREMY 62
QY 70 AVKRIANAFDIYMDAKRTLRREIKLRHLDHENVIGLRDVIPLRPFESDVYIAELMDT 129
DB 63 AIKRIANAFDNMOKAKRLREIKLRHLDHENVIGLRDVIPLRPFESDVYIAELMDT 122
QY 130 DLHQIIRSNQGLSEDCQYFMYQLLRGLKYIHSANVLRHDLKPSNMLLVANCDLKICDFG 189
DB 123 DLHNIIRSNQGLSEDCQYFMYQLLRGLKYIHSANVLRHDLKPSNMLLVANCDLKICDFG 182
QY 190 LARPPIENMTEYVYTWYRAPPELLNSSDYTAIDWVSGCITMELNKRPLRGKDH 249
DB 183 LARPSSEDDMMTEYVYTWYRAPPELLNSTDYSAIDWVSGCITMELNKRPLRGKDH 242
QY 250 VHOIRLTELGTPTADLGLFQNEADAKRYIRQLPQHRQOLAEEFPHVNPALIDLVMK 309
DB 243 MHQMLLIEVIGTPTDDDLGFRINEDARVMHRLQFRRRRPRGQPRKYQAPALDILEM 302
QY 310 LTFDPTIRITVEALRDHYLAKLHDAGDEPICVPFSEDFEOGIGEOIKIMYQOALS 369
DB 303 LTFNDRITVEALEHLYERLHDVADERICDTSFDFEQHPLTEDOMKQILNEALE 362
QY 370 LNPEY 374
DB 363 LNPNF 367

RESULT 13
Q9ZMJ5 PRELIMINARY; PRT; 399 AA.
AC Q9ZMJ5;
DT 01-MAY-1999 (TReMBLrel. 10, Created)

DT 01-MAY-1999 (TReMBLrel. 10, last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, last annotation update)
DE MAP kinase 5.
GN ZMMPK5.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoidae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HONEYBUNTAM;
RX MEDLINE=20055759; PubMed=10589842;
RA Berberich T., Sano H., Kusano T.;
RT "Involvement of a MAP kinase, ZmMPK5, in senescence and recovery from
RT low-temperature stress in maize.";
RL Mol. Gen. Genet. 262:534-542(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB016802; BAA74734.1; -.
DR HSSP: P27703; 1ERK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Prodom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SO SEQUENCE 399 AA; 44891 MW; 04982715587106C9 CRC64;

Query Match 74.1%; Score 1472.5; DB 10; Length 399;
Best Local Similarity 71.2%; Pred. No. 1.1e-117;
Matches 277; Conservative 45; Mismatches 50; Indels 17; Gaps 4;
QY 1 MADAMNAGCGGQFPDP-----SVLTHGGQYQVDFGCFNFETTKYRPPI 46
DB 12 MEAGAGG-GGGQPPQOPLRPVGGYVMDNIQATLSHGCFIOYNIFGNVFEYTAKKPPL 70
QY 47 MDIGRGAGYGVCSVINTL-LENMVAVKRIANAFDIYMDAKRTLRREIKLRHLDHENVIGL 105
DB 71 LPIGRGAGYGVCSAVNSEFAAGGSPSKRIANAFDNKIDAKRLRREIKLRHMDHENVIAI 130
QY 106 RDVIPLRPFESDVYIAELMDTDLHQIIRSNQGLSEDCQYFMYQLLRGLKYIHSANV 165
DB 131 RDIIPPQAAPADNDVYIAELMDTDLHQIIRSNQGLSEDCQYFMYQLLRGLKYIHSANV 190
QY 166 LHRDLKPSNMLLVANCDLKICDFGLARPIENENMTEYVYTWYRAPPELLNSSDYTAI 225
DB 191 LHRDLKPSNMLLVANCDLKICDFGLARPTSTEDPMTEYVYTWYRAPPELLNSSDYTAI 250
QY 226 DWVSVGCIPTMELNKRPLRGKDHVHOIRLTELGTPTADLGLFQNEADAKRYIRQLP 285
DB 251 DWVSVGCIPTMELNKRPLRGKDHVHOIRLTELGTPTADLGLFQNEADAKRYIRQLP 309
QY 286 HPRQOLAEEFPHVNPALIDLVMKLTPTDPTIRITVEALRDHYLAKLHDAGDEPICVPF 345
DB 310 HPRQSLPEKFRVNPALIDLVMKLTPTDPTIRITVEALRDHYLAKLHDAGDEPICVPF 369
QY 346 SPDFEOGIGEOIKIMYQOALSINPEY 374
DB 370 SPDFEOHALSEBQMDLITQOALANPDY 398

RESULT 14
Q9FSE6 PRELIMINARY; PRT; 369 AA.
AC Q9FSE6;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE MAPK2 protein.

GenCore version 5.1.5
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OM protein - protein search, using sw model

Run on: May 20, 2003, 00:20:45 ; Search time 35 seconds
(without alignments)
315.246 Million cell updates/sec

Title: US-09-623-034-2
Perfect score: 1987
Sequence: 1 MADANMGAGCGFPDPFSLV.....EEQIKDMYOEALSLNPEYA 375

Scoring table:
BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_patents_AA:*

- 1: /cgn2_6/p/odata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/p/odata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_6/p/odata/2/1aa/6A_COMB.pep.*
- 4: /cgn2_6/p/odata/2/1aa/6B_COMB.pep.*
- 5: /cgn2_6/p/odata/2/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/p/odata/2/1aa/backfillsl.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1987	100.0	375	2	US-08-837-593-5	Sequence 5, Appli
2	1661	83.6	370	2	US-08-837-593-7	Sequence 7, Appli
3	1634	82.2	371	2	US-08-837-593-6	Sequence 6, Appli
4	1509	75.9	393	2	US-08-837-593-3	Sequence 3, Appli
5	1500.5	75.5	387	2	US-08-837-593-4	Sequence 4, Appli
6	1482	74.6	393	2	US-08-837-593-2	Sequence 2, Appli
7	1292	65.0	371	2	US-08-837-593-8	Sequence 8, Appli
8	1094.5	55.1	372	2	US-08-837-593-9	Sequence 9, Appli
9	950	47.8	304	4	US-09-739-455-13	Sequence 13, Appli
10	950	47.8	304	4	US-09-739-455-23	Sequence 23, Appli
11	886.5	44.6	380	3	US-08-459-953A-9	Sequence 9, Appli
12	885.5	44.6	415	1	US-08-176-620A-4	Sequence 4, Appli
13	885.5	44.6	415	1	US-08-463-862-4	Sequence 4, Appli
14	885.5	44.6	415	2	US-08-461-985-4	Sequence 4, Appli
15	885.5	44.6	415	2	US-08-458-887-4	Sequence 4, Appli
16	885.5	44.6	415	4	US-08-932-787B-4	Sequence 4, Appli
17	885.5	44.6	415	4	US-08-932-012C-4	Sequence 4, Appli
18	885.5	44.6	415	4	US-08-888-818C-4	Sequence 4, Appli
19	878.5	44.2	360	4	US-09-457-040B-3	Sequence 3, Appli
20	878.5	44.2	365	1	US-08-176-620A-2	Sequence 2, Appli
21	878.5	44.2	365	1	US-08-463-862-2	Sequence 2, Appli
22	878.5	44.2	365	2	US-08-461-985-2	Sequence 2, Appli
23	878.5	44.2	365	2	US-08-458-887-2	Sequence 2, Appli
24	878.5	44.2	365	4	US-08-932-787B-2	Sequence 2, Appli
25	878.5	44.2	365	4	US-08-932-012C-2	Sequence 2, Appli
26	878.5	44.2	365	4	US-08-888-818C-2	Sequence 2, Appli
27	878.5	44.2	367	1	US-08-176-620A-11	Sequence 11, Appli

28	878.5	44.2	367	2	US-08-461-985-11	Sequence 11, Appli
29	877.5	44.2	358	1	US-08-176-620A-12	Sequence 12, Appli
30	877.5	44.2	358	2	US-08-461-985-12	Sequence 12, Appli
31	877.5	44.2	358	4	US-09-457-040B-4	Sequence 4, Appli
32	877.5	44.2	360	3	US-08-622-277A-14	Sequence 14, Appli
33	877.5	44.2	364	4	US-09-457-040B-34	Sequence 34, Appli
34	872	43.9	379	4	US-09-411-628-14	Sequence 14, Appli
35	870	43.8	353	1	US-08-176-620A-14	Sequence 14, Appli
36	870	43.8	353	2	US-08-461-985-14	Sequence 14, Appli
37	867	43.6	379	4	US-09-025-580-25	Sequence 25, Appli
38	864.5	43.5	355	3	US-08-459-953A-8	Sequence 8, Appli
39	864.5	43.5	360	4	US-09-457-040B-35	Sequence 35, Appli
40	863.5	43.5	365	4	US-09-025-580-2	Sequence 2, Appli
41	860	43.3	379	3	US-08-622-277A-8	Sequence 8, Appli
42	849	42.7	353	4	US-08-932-787B-19	Sequence 19, Appli
43	849	42.7	353	4	US-08-932-012C-19	Sequence 19, Appli
44	849	42.7	353	4	US-08-888-818C-19	Sequence 19, Appli
45	841	42.3	360	1	US-08-674-612-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-837-593-5
; Sequence 5, Application US/08837593
; Patent No. 5977442
; GENERAL INFORMATION:
; APPLICANT: Kleesig, Daniel F.
; APPLICANT: Zhang Zhigun
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; ADDRESS: P. C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,593
; FILING DATE: April 21, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,805
; FILING DATE: October 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; TELE: INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-837-593-5

Query Match 100.0%; Score 1987; DB 2; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.2e-200;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MADANMGAGGCGPPDPFVSVLTHGGQYVQFDIFGNFEITTKYRPPIMPIGAGYICVSV 60
DB 1 MADANMGAGGCGPPDPFVSVLTHGGQYVQFDIFGNFEITTKYRPPIMPIGAGYICVSV 60
QY 61 LNTLNMVAVKRIANAFDIYMDAKRTLREIKLRHLDHENYIGLRVYIPPLRERSDV 120
DB 61 LNTLNMVAVKRIANAFDIYMDAKRTLREIKLRHLDHENYIGLRVYIPPLRERSDV 120
QY 121 YATLMDTDLHQIIRSNOSLSEDCQYFMVQLRGLKXIHSAVNLHRDLKPSNLLVYAN 180
DB 121 YATLMDTDLHQIIRSNOSLSEDCQYFMVQLRGLKXIHSAVNLHRDLKPSNLLVYAN 180
QY 181 CDKICDFGLARPIENENMTYVYTRAPPELLNSTDYTAIDVWSGCIPELMNR 240
DB 181 CDKICDFGLARPIENENMTYVYTRAPPELLNSTDYTAIDVWSGCIPELMNR 240
QY 241 KPLFGGDHVOIRLLELTGTPEADLGFQNEADAKRYIRQLPQHPROQLAEYFPHVNP 300
DB 241 KPLFGGDHVOIRLLELTGTPEADLGFQNEADAKRYIRQLPQHPROQLAEYFPHVNP 300
QY 301 LAIDLVDKMLTFDPTRITVEALDHPYLAKLHDAGDEPICVPVPSFDEQOIGEBQIK 360
DB 301 LAIDLVDKMLTFDPTRITVEALDHPYLAKLHDAGDEPICVPVPSFDEQOIGEBQIK 360
QY 361 DMVIOEALSLNPEYA 375
DB 361 DMVIOEALSLNPEYA 375

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RESULT 2 US-08-837-593-7

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; Sequence 7, Application US/08837593
; Patent No. 5977442
; GENERAL INFORMATION:
; APPLICANT: Klessig, Daniel F.
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plant
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,593
; FILING DATE: April 21, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,805
; FILING DATE: October 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; US-08-837-593-7

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Query Match 83.6%; Score 1661; DB 2; Length 370;
 Best Local Similarity 82.4%; Pred. No. 2.4e-166;
 Matches 304; Conservative 36; Mismatches 29; Indels 0; Gaps 0;

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QY 6 MGAGGCGPPDPFVSVLTHGGQYVQFDIFGNFEITTKYRPPIMPIGAGYICVSVLTEL 65
DB 1 MNTGGGQYTFPAVDTHGGQYVQFDIFGNFEITTKYRPPIMPIGAGYICVSVLTEL 60
QY 66 NEMVAVKRIANAFDIYMDAKRTLREIKLRHLDHENYIGLRVYIPPLRERSDVYATL 125
DB 61 NEMVAVKRIANAFDIYMDAKRTLREIKLRHLDHENYIGLRVYIPPLRERSDVYATL 120
QY 126 LMDTDLHQIIRSNOSLSEDCQYFMVQLRGLKXIHSAVNLHRDLKPSNLLVYANCDLKI 185
DB 121 LMDTDLHQIIRSNOSLSEDCQYFMVQLRGLKXIHSAVNLHRDLKPSNLLVYANCDLKI 180
QY 186 CDFGLARPIENENMTYVYTRAPPELLNSTDYTAIDVWSGCIPELMNRKPLFG 245
DB 181 CDFGLARPIENENMTYVYTRAPPELLNSTDYTAIDVWSGCIPELMNRKPLFG 240
QY 246 GKDHVOIRLLELTGTPEADLGFQNEADAKRYIRQLPQHPROQLAEVPHVNPALIDL 305
DB 241 GKDHVOIRLLELTGTPEADLGFQNEADAKRYIRQLPQHPROQLAEVPHVNPALIDL 300
QY 306 VDKMLTFDPTRITVEALDHPYLAKLHDAGDEPICVPVPSFDEQOIGEBQIKMDIXQ 365
DB 301 VDKMLTFDPTRITVEALDHPYLAKLHDAGDEPICVPVPSFDEQOIGEBQIKMDIXQ 360
QY 366 EALSLNPEY 374
DB 361 EALSLNPEY 369

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RESULT 3

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; Sequence 6, Application US/08837593
; Patent No. 5977442
; GENERAL INFORMATION:
; APPLICANT: Klessig, Daniel F.
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in P
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,593
; FILING DATE: April 21, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: 60/029,805
FILING DATE: October 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: Rutgers 97-0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-837-593-6

Query Match 82.2%; Score 1634; DB 2; Length 371;
Best Local Similarity 82.8%; Pred. No. 1,66-163;
Matches 299; Conservative 38; Mismatches 24; Indels 0; Gaps 0;

QY 15 DPSPVLTGGQYVQDFDIGNFPEITTKRPPIMPGRGAYGIVSVLTNEMVAVKKI 74
DB 11 EFPAVQTHGGQYVQYVNGNLFEEVAKYRPPIMPGRGAYGIVSVLTNEMVAVKKI 70
QY 75 ANAFDIYMDAKRTLEIKLRHLHDEHENVIGLDVIRPPRRFSPVYATLMDTDLHQI 134
DB 71 ANAFDINHDAKRTLEIKLRHLHDEHENVIGLDVIRPPRRFNDVYITTEMDTDLHQI 130
QY 135 IRSNOGLSEDCQYPMYOLLRLGLKYIHSANVLHRDLKPSNLLVYANCIDKICFGLARP 194
DB 131 IRSNOGLSEDCQYPMYOLLRLGLKYIHSANVLHRDLKPSNLLVYANCIDKICFGLARP 190
QY 195 IENEMTEYVYTRWYRAPELNLNSDYTAIDVWSVGCIFMELMNRKPLFGKDHVHQR 254
DB 191 MESDMTEYVYTRWYRAPELNLNSDYTAIDVWSVGCIFMELMNRKPLFGKDHVHQR 250
QY 255 LTELGLPTTEADLGLFONEDAKRYIRQLPQHRQOAEVFPVHNPALDLDVKMLTDP 314
DB 251 LTELGLPTTEADLGLFONEDAKRYIRQLPQHRQOAEVFPVHNPALDLDVKMLTDP 310
QY 315 TRRTVEALDHPYLAKLHDAGDEPICVPFSEFDEOQIGEEQIKDMITQALSNPEY 374
DB 311 TRRTVEALDHPYLAKLHDAGDEPICVPFSEFDEOQIGEEQIKDMITQALSNPEY 370
QY 375 A 375
DB 371 A 371

RESULT 4
US-08-837-593-3
Sequence 3, Application US/08837593
Patent No. 5977442
GENERAL INFORMATION:
APPLICANT: Klessig, Daniel F.
TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
ADDRESS: P.C.
STREET: 1601 Market Street, Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: United States of America

ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,593
FILING DATE: April 21, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,805
FILING DATE: October 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: Rutgers 97-0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-837-593-3

Query Match 75.9%; Score 1509; DB 2; Length 393;
Best Local Similarity 72.6%; Pred. No. 2,5e-150;
Matches 278; Conservative 44; Mismatches 49; Indels 12; Gaps 2;

QY 3 DANMAGGQGP-----DPSVLTGGQYVQDFDIGNFPEITTKRPPIMP 51
DB 9 DTVMSDAAQOPAPPSQYAGIDNIPATLSHGREFQYVIFENIEVAKYRPPIMP 68
QY 52 GAYGIVSVLTNEMVAVKKIANAADYMDAKRTLEIKLRHLHDEHENVIGLDVIRPP 111
DB 69 GAYGIVSVLTNEMVAVKKIANAADYMDAKRTLEIKLRHLHDEHENVIGLDVIRPP 128
QY 112 PLRREFSDVYIATLMDTDLHQIIRSNOGLSEDCQYPMYOLLRLGLKYIHSANVLHRDLK 171
DB 129 POREAFNDVYIATLMDTDLHQIIRSNOGLSEDCQYPMYOLLRLGLKYIHSANVLHRDLK 188
QY 172 PSNLLVYANCIDKICFGLARPNIENEMTEYVYTRWYRAPELNLNSDYTAIDVWSVG 231
DB 189 PSNLLVYANCIDKICFGLARPNIENEMTEYVYTRWYRAPELNLNSDYTAIDVWSVG 248
QY 232 CIFMELMNRKPLFGKDHVHQRILTELGLPTTEADLGLFONEDAKRYIRQLPQHRQO 291
DB 249 CIFMELMNRKPLFGKDHVHQRILTELGLPTTEADLGLFONEDAKRYIRQLPQHRQO 307
QY 292 AEVFPVHNPALDLDVKMLTFDPTTRITVEALDHPYLAKLHDAGDEPICVPFSEFDEO 351
DB 308 VEKFPVHNPALDLDVKMLTFDPTTRITVEALDHPYLAKLHDAGDEPICVPFSEFDEO 367
QY 352 QGIGEEQIKDMITQALSNPEY 374
DB 368 HALTEQMKELIYRGLAFNP 390

RESULT 5
US-08-837-593-4
Sequence 4, Application US/08837593
Patent No. 5977442
GENERAL INFORMATION:
APPLICANT: Klessig, Daniel F.

APPLICANT: Zhang Zhugun
TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plant
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
ADDRESSEE: P.C.
STREET: 1601 Market Street, Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: United States of America
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,593
FILING DATE: April 21, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,805
FILING DATE: October 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: Rutgers 97-0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-08-837-593-4

Query Match 75.5%; Score 1500.5; DB 2; Length 387;
Best Local Similarity 74.3%; Pred. No. 1.9e-149;
Matches 278; Conservative 43; Mismatches 52; Indels 1; Gaps 1;
QY 1 MADANMAGGQPPDFPSVLTGSGQYQVDFGFFETTKYRPPIMPICGAGYICSV 60
DB 13 MSDAAPAPQMGJENIPAVLSHGGRFIOYNIFEVTAKKPIMPICGAGYICSA 72
QY 61 LNFELNEMVAVKRIANAFDIYMDAKRTLRKILRLHLDHENVIGLRDVIPIPLRRESDV 120
DB 73 HNSTETNHAVAKRIANAFDNDKIDAKRTLRKILRLHMDHENVAVAKRIIVPPORRENDV 132
QY 121 YIATELMDTDLHQIIRSNQGLSEDHCOYFMQVQLRGLKYLHSANVLRDLKPSMLNAN 180
DB 133 YIATELMDTDLHQIIRSNQGLSEDHCOYFLYQLRGLKYLHSANVLRDLKPSMLNAN 192
QY 181 CDLKCIFGLARPNIEENMTETVYVTRWYRAPPELLNSSDYTAIDVWSGCIPELMNR 240
DB 193 CDLKCIFGLARPNIEENMTETVYVTRWYRAPPELLNSSDYTAIDVWSGCIPELMNR 252
QY 241 KPLEGGDHYHOIRLLELLGTEADLGLQNEADAKRYRQLPQHRRQOLAEFPRVNP 300
DB 253 KPLEGGDHYHOIRLLELLGTEADLGLQNEADAKRYRQLPQHRRQOLAEFPRVNP 311
QY 301 LAIDLVMKMLTFDPTRITVEEALDHPYLAKLHDAGDEPICVPFSEDFEQOGIGEQIK 360
DB 312 LAIDLVMKMLTFDPTRITVEEALDHPYLAKLHDAGDEPICVPFSEDFEQOGIGEQIK 371

QY 361 DMIVQALSLNPEY 374
DB 372 ELIYREALAFNPEY 385

RESULT 6
US-08-837-593-2
Sequence 2, Application US/08837593
Patent No. 5977442
GENERAL INFORMATION:
APPLICANT: Klesid, Daniel F.
TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in P
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
ADDRESSEE: P.C.
STREET: 1601 Market Street, Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: United States of America
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,593
FILING DATE: April 21, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,805
FILING DATE: October 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: Rutgers 97-0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-08-837-593-2

Query Match 74.6%; Score 1482; DB 2; Length 393;
Best Local Similarity 71.5%; Pred. No. 1.7e-147;
Matches 274; Conservative 46; Mismatches 51; Indels 12; Gaps 2;
QY 3 DANMAGGQPP-----DFPSVLTGSGQYQVDFGFFETTKYRPPIMPICR 51
DB 9 DTMMSDAGARQPPAPQVAGMDNIPATLSHGGRFIOYNIFEVTAKKPILPICK 68
QY 52 GAGIVGCVNTELENVAVAKRIANAFDIYMDAKRTLRKILRLHLDHENVIGLRDVIPI 111
DB 69 GAGIVGCVNTELENVAVAKRIANAFDNDKIDAKRTLRKILRLHMDHENVAVARDTIIP 128
QY 112 PLRREFSDYIATELMDTDLHQIIRSNQGLSEDHCOYFMQVQLRGLKYLHSANVLRDLK 171
DB 129 PQRARFNDYIATELMDTDLHQIIRSNQGLSEDHCOYFLYQLRGLKYLHSANVLRDLK 188
QY 172 PSNLLVANCDLKCIFGLARPNIEENMTETVYVTRWYRAPPELLNSSDYTAIDVWSG 231

Db	189	PSNLLNANDCLKICDDEGLARVSETEOPMEIYVTRRYRREPELLINSDDTAADWASVG	248
Qy	232	CIFELMANKRPLEGCKQHVHOIRLTELLEGTPTPEADIGFQUNEDAKRYIROLDOPHPOOL	291
Db	249	CIFELMDRKLPEFGRHVHOLRIIMELIGPSEAEKEEFL-NEAKRKYIRQLDPLYRROSF	307
Qy	292	AEEVPHNPLAIDLVDKMLTFDPRTRTTVEALDHPRLAKIHQAGDPCIVPVSFPFEO	351
Db	308	TEKPRHHPRLAIDLVEKMLTFDPRRRTITVEGALAHPLNLSHDSIDPRTCMTPSPFDEQ	367
Qy	352	QGIGEEQIKMDIYOALSNDEY	374
Db	368	HALTEEQMKELIYRESLAFNDEY	390

RESULT 7
US-08-837-593-8
Sequence 8, Application US/08837593
Patent No. 5977442
GENERAL INFORMATION:
APPLICANT: Klessig, Daniel F.
APPLICANT: Zhang Zhun
TITLE OF INVENTION: No. 5977442el Salicylic Acid Induced
TITLE OF INVENTION: Map Kinase and Its Use for Enhanced Disease Resistance in Plant

Query March	65.0%	Score 1292;	DB 2;	Length 371;
Best Local Similarity	62.8%	Pred. No. 1.5e-12/;		
Matches 225; Conservative	70;	Mismatches 63;	Indels 0;	Gaps 0;

Db	10	EIKGIPTHEKYYEYVAVLGNFEVYSKTIIPPIQVYGGATGMCAGANSSETKEVAIKKI	69
Qy	75	ANAFDIYMDAKKTAREIKLLRLHLDHENYIGLRDVIPEPLRRESDVIATELMDTDLHOI	13
Db	70	GNAFENRIDAKPTLRLEIKLISHMDHENIETIKIDIVPPDPRREFEENDYIYVELMDTDLHOI	12
Qy	135	IRSNQGSSEDCOCPYAYOLLRGKTIKHSANVLRHDLKPSNLVYANCDLKICDFGLARPN	19
Db	130	IRSSQALITEDHCQYFLYOLLRGKTIKHSANVLRHDLKPSNLVYANCDLKICDFGLARTT	18
Qy	195	IENENMETEYVYTWYRAPPELLNSSDYTAIDVMSVGCIPMEIMLNRRKPLFGKGDHYQIR	25
Db	190	SEADFMETEYVYTWYRAPPELLNCTEYTAADIMSVGCIIMELIKREPLFPGRDYAOQDG	24
Qy	255	LITELIGTPEALDGLQWEDAKRTIRQLPOHPOQLAEVPHNPPLAIDVLYKMTLTPD	31
Db	250	LITALLQSPEDSLGTRBDNRKAKYKHLPRVPHRPPSQKFPDYSLAIDLARMLVFPD	30
Qy	315	TRRIYVEALDHPYLAKLHDADGDEPTCFVPPSPDFDEOOGIGEBQIKDVIQEALSLNP	372
Db	310	AKRITVEDALANHPFLLSHEINIEEYVCSPPNPFDEASSEDQIKELINNEALAKDP	367

RESULT 8
US-08-837-593-9
: Sequence 9, Application US/08837593


```
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,953A
FILING DATE: June 2, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,494
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/267
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9 :
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-953A-9
```

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Query Match          44.6%; Score 886.5; DB 3; Length 380;
Best Local Similarity 46.5%; Pred. No. 7.1e-85;
Matches 174; Conservative 73; Mismatches 114; Indels 13; Gaps 7;
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QY 7 GAGGQGFDFPSVLTGG--QYVQDFDIGNFETTKYRPPIMPIGRGAYGVCSVLNTE 64
DB 12 GGGGSPAAANMAAAAGAPENVR---GQVFDVGPRT-TNLSYIGEGAYGVCSAYDNV 66
QY 65 LNEAVAKIANAFIDYMDAKRTLRKILRLDHEENVGLRDVIRPPLRREFSDVIAT 124
DB 67 NKVRRAIKKI-SPEFHQYTCQRTLRKILRFRHENIIGINDIIQAPRTIEQMKDYIYQ 125
QY 125 ELMQDTLHQIIRSNQGLSEDCQYFMVQLRGKLYIHSANVLRDLKPSNLLVNAKDLK 184
DB 126 DLMETDLKYLKLT-OHLSNDHICFLYQILRGKLYIHSANVLRDLKPSNLLNTCDLK 184
QY 185 ICDPEFLAR---PNIENEN-MTEYVYTRWYRAPPELLNSDYTAADVWVGCIPEMLNR 240
DB 185 ICDPEFLARADDDHDTGFLTEYVATRWYRAPELMINSGYKSIDIVSGCIIAEMLSN 244
QY 241 KPLFGKDVHQIRLTTELLGTPTTEADLGFQINEDAKRYIRQLPQHPROQLAEVPPHVP 300
DB 245 RPIFGKHYLDQNLHILGLISPSQEDLNCIINLKARNYLLSLPHKNKYPWNRLEPNADS 304
QY 301 LAIDLVDKMLTFDPTTRITVEBALDHPYLAKLHDAGDEPICPVPSFDEQOIGEEQIK 360
DB 305 KALDLDKMLTFNPHKRIEVEQALAHPLYLEQYDPSDEPIAEAPFKFDMELDLDPKEXLK 364
QY 361 DMIVQEALSLNPEY 374
DB 365 ELIFEETARPOPGY 378
```

```
RESULT 12
US-08-176-620A-4
Sequence 4, Application US/08176620A
Patent No. 5595904
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Nye, Steven
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
```

```
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,620A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4 :
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-176-620A-4
```

```
Query Match          44.6%; Score 885.5; DB 1; Length 415;
Best Local Similarity 46.8%; Pred. No. 1e-84;
Matches 173; Conservative 73; Mismatches 113; Indels 11; Gaps 6;
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QY 9 GGGQPPDFPSVLTTHGGVQDFDIGNFETTKYRPPIMPIGRGAYGVCSVLNTELMEM 68
DB 51 GGGCANAANMAAAAGAPENVR----GQVFDVGPRT-TNLSYIGEGAYGVCSAYDNVNR 105
QY 69 YAVKRIANAFIDYMDAKRTLRKILRLDHEENVGLRDVIRPPLRREFSDVIATLEMD 128
DB 106 VAIKKI-SPEFHQYTCQRTLRKILRFRHENIIGINDIIAPRTIEQMKDYIYQDLME 164
QY 129 TDLHQIIRSNQGLSEDCQYFMVQLRGKLYIHSANVLRDLKPSNLLVNAKDLKICDF 188
DB 165 TDLVYLKLT-OHLSNDHICFLYQILRGKLYIHSANVLRDLKPSNLLNTCDLKICDF 223
QY 189 GLAR---PNIENEN-MTEYVYTRWYRAPPELLNSDYTAADVWVGCIPEMLNRKPLF 244
DB 224 GLARVADDDHDTGFLTEYVATRWYRAPELMINSGYKSIDIVSGCIIAEMLSNRPLE 283
QY 245 GSKDENVHQIRLTTELLGTPTTEADLGFQINEDAKRYIRQLPQHPROQLAEVPPHVP 304
DB 284 PEKHYLDQNLHILGLISPSQEDLNCIINLKARNYLLSLPHKNKYPWNRLEPNADSKALD 343
QY 305 LVDKMLTFDPTTRITVEBALDHPYLAKLHDAGDEPICPVPSFDEQOIGEEQIKDMY 364
DB 344 LLDKMLTFNPHKRIEVEQALAHPLYLEQYDPSDEPIAEAPFKFDMELDLDPKEXLELIF 403
QY 365 QEALSLNPEY 374
DB 404 EETARPOPGY 413
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```
RESULT 13
US-08-463-862-4
Sequence 4, Application US/08463862
Patent No. 5776751
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G. et al.
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
```

```

: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/463,862
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/701,544
: FILING DATE: 16-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Mistrock, S. Leslie
: REGISTRATION NUMBER: 18,872
: REFERENCE/DOCKET NUMBER: 6526-049
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 790-9090
: TELEFAX: 212 869-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 415 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-463-862-4

```

```

Query Match          44.6%; Score 885.5; DB 1; Length 415;
Best Local Similarity 46.8%; Pred. No. 1e-84;
Matches 173; Conservative 73; Mismatches 113; Indels 11; Gaps 6;

```

```

OY 9 GGGGPPDPSPVLTTHGGGVQDFDIGNFFETTKRPPIMPGRAYGVCVLTNLENM 68
DB 51 GGGCAANNAANAAAAAGPEVVR---GOVFDVGPRY-TNLSYIGEGAYGVCAYDNLKVR 105
OY 69 VAVKRIANAFDIYMDAKRTLEIKILRLHDHENYIGLDVTPPLRREPSDVIATLEMD 128
DB 106 VAIKRI-SPEFHQTYCQRTLEIKILRLFRHENITIGINDIRAPTIEMKADVIYVDLME 164
OY 129 TDLHQIIRNSOGLSEDCQYFMYLRLGKLYHSANVLRDLKPSNLLVYANCDLKTICDF 188
DB 165 TDLKRLKT-OHLSNDHCYFLYQILRLGKLYHSANVLRDLKPSNLLVYANCDLKTICDF 223
OY 189 GLAR---PNIENEN-MTEYVYTRMYRAPELLNSDYTAIDVWSVGCIFMELNKRPLF 244
DB 224 GLARVADPDHDHTGFLTEYVATRYRAPEIMLNSKGYTKSIDIVSVCILAEMLSNRPITF 283
OY 245 GKKDHVHQIRLLTTEADLGFLONEDAKRYIRQLPOHPRQOLAEVPPHNPPLAID 304
DB 284 PKRHYLDQNLHIILGILSPSEDNLNCIINLKARNTLSLPRKKNVPMNRRLFPNDSKALD 343
OY 305 LVDKMLTFDPTRITVEALDHPYLAKLHDAGDEPICVPSPFDEOOGIGEEOIKDMY 364
DB 344 LLDKMLTFNPKRIEVBQALAHPLYEQYDPSDEPIAEAPKFMELDIDLPRKELKELIF 403
OY 365 QEALSLNPEY 374
DB 404 EETARFQPGY 413

```

```

RESULT 14
: Sequence 4, Application US/08461985
: Patent No. 5872006
: GENERAL INFORMATION:
: APPLICANT: Boulton, Teri G.
: APPLICANT: Cobb, Melanie H.
: APPLICANT: Yancopoulos, George D.
: APPLICANT: Nye, Steven

```

```

: APPLICANT: Panayotatos, Nikos
: TITLE OF INVENTION: A Family of Map2 Protein Kinases
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/461,985
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/176,620
: FILING DATE: 03-JAN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Mistrock, S. Leslie
: REGISTRATION NUMBER: 18,872
: REFERENCE/DOCKET NUMBER: 6526-123
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 415 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-461-985-4

```

```

Query Match          44.6%; Score 885.5; DB 2; Length 415;
Best Local Similarity 46.8%; Pred. No. 1e-84;
Matches 173; Conservative 73; Mismatches 113; Indels 11; Gaps 6;

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```

OY 9 GGGGPPDPSPVLTTHGGGVQDFDIGNFFETTKRPPIMPGRAYGVCVLTNLENM 68
DB 51 GGGCAANNAANAAAAAGPEVVR---GOVFDVGPRY-TNLSYIGEGAYGVCAYDNLKVR 105
OY 69 VAVKRIANAFDIYMDAKRTLEIKILRLHDHENYIGLDVTPPLRREPSDVIATLEMD 128
DB 106 VAIKRI-SPEFHQTYCQRTLEIKILRLFRHENITIGINDIRAPTIEMKADVIYVDLME 164
OY 129 TDLHQIIRNSOGLSEDCQYFMYLRLGKLYHSANVLRDLKPSNLLVYANCDLKTICDF 188
DB 165 TDLKRLKT-OHLSNDHCYFLYQILRLGKLYHSANVLRDLKPSNLLVYANCDLKTICDF 223
OY 189 GLAR---PNIENEN-MTEYVYTRMYRAPELLNSDYTAIDVWSVGCIFMELNKRPLF 244
DB 224 GLARVADPDHDHTGFLTEYVATRYRAPEIMLNSKGYTKSIDIVSVCILAEMLSNRPITF 283
OY 245 GKKDHVHQIRLLTTEADLGFLONEDAKRYIRQLPOHPRQOLAEVPPHNPPLAID 304
DB 284 PKRHYLDQNLHIILGILSPSEDNLNCIINLKARNTLSLPRKKNVPMNRRLFPNDSKALD 343
OY 305 LVDKMLTFDPTRITVEALDHPYLAKLHDAGDEPICVPSPFDEOOGIGEEOIKDMY 364
DB 344 LLDKMLTFNPKRIEVBQALAHPLYEQYDPSDEPIAEAPKFMELDIDLPRKELKELIF 403
OY 365 QEALSLNPEY 374
DB 404 EETARFQPGY 413

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RESULT 15
: US-08-458-887-4

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Search completed: May 20, 2003, 00:25:17
Job time : 36 secs

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; Sequence 4, Application US/08458887
; Patent No.: 5914261
; GENERAL INFORMATION:
; APPLICANT: Boulton, Teri G. et al.
; TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,887
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,544
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-887-4

Query Match 44.6%; Score 885.5; DB 2; Length 415;
Best Local Similarity 46.8%; Pred. No. 1e-84;
Matches 173; Conservative 73; Mismatches 113; Indels 11; Gaps 6;

QY 9 GGGGPPDPSPVLTTHGGVYQFDIFGNFPEITTKYRPPIMPICRGAYIVCSVLTNELNEM 68
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 51 GGGCANMAAAGPEMYR--GQVFDVGPY-TNLSYIGEGAYGMVCSAYDMLNKYR 105

QY 69 VAVKRIANAFDIYMDAKRTLRREIKLRLHLDHENVIGLRDVIPPLRREFSDVYIATELMD 128
   |||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 106 VAIKRI-SPEHQYTCQRTLRREIKLRLFRHNIIGINDIIRAPITIEQMKDYIYQDLME 164

QY 129 TDLHOITRSNCGLEDHCQYFYQLRLGLKTYHSANVLHRLDKPSNLLVANCCLKICDF 188
   |||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 165 TDLVYKRLKT-OHLSDNHICYFLYQILRGKTYHSANVLHRLDKPSNLLVANCCLKICDF 223

QY 189 GLAR---PNIENEN-MTEYVYVTRWRAPPELLNSSDYTAIDVMSVGCIFMELMNRKPLF 244
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 224 GLARVADPDHDTGFTLEVATRWTRAPETIMLSKGYTKSIDVMSVGCILAEMLSNRPLF 283

QY 245 GKKDHVHQLRLTELLGTPTTEADLGLQNEADAKRYIRQLPQHPROOLAEVPPHVNPLAID 304
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 284 PKHYLDQNLNHLIGLSPSQEDLNCITNLKARNYLLSLPHKNKYPMWNRLLFPNADSKALD 343

QY 305 LVDKMLTFDPTRRTTYEELDHPYLAKLHDAGDEPICVPYPSFDFEQGIGEEQIKDMTY 364
   |||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 344 LLDKMLTFNPKRIEVEQALAHPLYLEQYYPSPDEPIAEAPFKFDWELDLPEKELKELIF 403

QY 365 QEALSLNPEY 374
   :| :|
Db 404 EETARFQPGY 413
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